



# ClustalW Results

Sequences Help

Ref: novel BLAST2 FASTA ClustalW GCG Assembly Prep Translation

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☐ GSEB\_AA55751  
☐ 103561CD1

## CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson  
Sequence 1: GSEB\_AA55751 2039 aa  
Sequence 2: 103561CD1 174 aa  
Start of Pairwise alignments  
Aligning...  
Sequences (1:2) Aligned. Score: 66  
Start of Multiple Alignment  
There are 1 groups  
Aligning...  
Group 1: Sequences: 2 Score:1942  
Alignment Score 710  
CLUSTAL-Alignment file created [baarka4ll.aln]  
CLUSTAL W (1.7) Multiple sequence alignment

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GSEB_AA55751      MGASSPSPPEVGPAPQGLPFCGGSLLAVVLLALPVAMGQNAPEMLPFAAPTNLTDE
103561CD1          -----MAPVRLERPFPRPFGLLAALVLLSSPDCVPEMLPFAAPTNLTMD
*
GSEB_AA55751      PEPPIGYLAVRCRGVSGRPSTICLNKSVWCAADRCRKSRRNPDPVNGAVHYTG
103561CD1          PEPPIGYLAVRCRGVSGRPSTICLNKSVWCAADRCRKSRRNPDPVNGAVHYTD
*
GSEB_AA55751      IOPGQIKYSCYGVRLIGSSANCIISGDTVWDMENPICDRIPCGLPPTITNGDFIST
103561CD1      IOPGQIKYSCYGVRLIGSSANCIISGDTVWDMENPICDRIPCGLPPTITNGDFIST
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GSEB_AA55751      NENPHYGSVVYTRCNPGSGGRKVPFELVGEBSITYCTSNDDVGWISGPAPOCIIPNKCTP
103561CD1      L-----
GSEB_AA55751      PAVENGILVSDNRSLFSLANEVVERFCQGFVMEGPRRVKCOALAKMEPELPSCSRVCQP
103561CD1      PAVENGILVSDNRSLFSLANEVVERFCQGFVMEGPRRVKCOALAKMEPELPSCSRVCQP
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GSEB_AA55751      PIVLAERTORDKDNFSPQGEVYVSCPEGYDLGAASLHCTPGQDWSPEAPRCAYVSCSD
103561CD1      PIVLAERTORDKDNFSPQGEVYVSCPEGYDLGAASLHCTPGQDWSPEAPRCAYVSCSD
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GSBQ_AAV55751 103561CD1	CPNPAILNGRHGTGSPSDIPYKKEISYTCDPHEDRGMTFNLIIGESTIRCTSDPHNGVW
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GSBQ_AAV55751 103561CD1	ENLWMSVIEDNCRKRSQPPPEPFGNANHINTDQGSTVWYSCNEGFRLLIGSPSTCYLV
GSBQ_AAV55751 103561CD1	SGNNVTMDKKAFIGELISCEPPPTISNGDPYSNNRSTSPHNGTVVTYQCHTGPDEQLFEL
GSBQ_AAV55751 103561CD1	VGBRSITCTSKDQVQWWSPPPRCISTNKCTAPEVENAIIVPQNSPFSULTEIIRRCQ
GSBQ_AAV55751 103561CD1	PGFVWVSGHTVQCQTNGRWGFKLPHCSRVCQPPPEILLGHEHTLSHQDNFSPQGEVYYSCE
GSBQ_AAV55751 103561CD1	PSYDLRGAASLHCTPQGDMSPEAPRCTVYSCDDELQQLPHGRVLLPLANQLGAKVSPVCD
GSBQ_AAV55751 103561CD1	EGFRUKGRSASHCVLAGKALMNSVIVCEQIIFCPNPAILNGRHGTGTFPGDIYKKEIS
GSBQ_AAV55751 103561CD1	YACDHPDPRGTFENLIGESSIRCTSDPQGNQWSSPAPRCELSTVPAACPHPEKIQNGHYI
GSBQ_AAV55751 103561CD1	GGHVSILYLPGMTISYTCDPGYLLVYGRGFIPTDQGLWSOLDHYCKEYNCSPPLFMNGISK
GSBQ_AAV55751 103561CD1	ELBEMKVTYHRYGDIYVTLKCEDEGYTLBGSFWSQCADDRMDPLACTSRAHDALIVGTLISG
GSBQ_AAV55751 103561CD1	TIFFILLIIFLSWILLKHKRGNNAHENPEVAIHLHSQGSVHPRTLQTNENSRLVP

Submit sequences to:



ID	AAV55751
CS	b6d742cf861fe7eeda126d4745a36eda
IDH	AAV55751 standard; Protein; 2039 AA.
MO	PRT
DV	PRT
D1	20-MAR-2003 (updated)
D2	22-FEB-2000 (first entry)
DT	PATENT US5981481-A
AK	PRIMARY AC AAV55751
AK	PRIMARY AC AAV55751
EAK	N-PSDB AAZ38150
DR	WPI 1999-63357/54
DR	Human C3b/C4b receptor (CRI) protein.
DE	Human C3b/C4b receptor (CRI) protein.
KM	Arthus reaction
KM	C3b/C4b receptor
KM	CRI protein
KM	autoimmune disorder
KM	cell-surface protein
KM	complement pathway enzyme
KM	complement regulatory activity
KM	diagnostic
KM	erythrocyte
KM	heart condition
KM	human
KM	inflammation
KM	myocardial infarct
KM	reperfusion injury
KM	tissue damage
EXM	
OS	Homo sapiens.
SC	4a22b9cfd6f59eca5a08e9eb4312eae
SP	HOMO SAPIENS
ESP	
INST	(AVAN-) AVANT IMMUNOTHERAPEUTICS INC
CC	The invention relates to a human C3b/C4b receptor (CRI) protein. The CRI protein or fragment is expressed as a cell-surface protein on the surface of a non-human cell and exhibits a complement regulatory activity in vivo -length human CRI as expressed on erythrocytes. The CRI function in vivo may be mediated through the inhibition of complement pathway enzymes. The soluble CRI protein exhibits a complement regulatory activity, and this may be used to prevent reperfusion injury, inhibit Arthus reaction, and neutrophil mediated tissue damage, and reduce myocardial infarct size, and inflammation. The CRI protein and its fragments can also be used in the treatment of conditions which involve unwanted complement activity, e.g. shock lung, tissue damage due to burn, or ischemic heart conditions, and autoimmune disorders. CRI proteins, analogues, derivatives, and anti-CRI antibodies are used in assays, and diagnostics. The present sequence represents the human CRI protein.
CC	(Updated on 20-MAR-2003 to correct PR field.)
ECG	
RC	1 f60f84ae97550b668750b6a74d037fed
RT	PD: 09-NOV-1999. PF: 06-JUN-1995; 95US-0470652. PR: 03-APR-1989; 89US-0332865. 24-FEB-1993; 93US-0026134. PR: 06-DEC-1994; 94US-0350238. PR: 01-APR-1988; 88U. A human C3b/C4b receptor (CRI) protein having antiinflammatory and cardiant ac Patent: US5981481-A. Disclosure; Fig 1A-P; 87dp; English.
RA	Concino M.F.
RA	Wong W.W.
RA	Makrides S.C.
RA	Klickstein L.B.
RA	Pearson D.T.
RA	IP S.H.
RA	Marsh H.C.
RA	Carson G.R.
RA	WONG WM
RA	MAKRIDES SC
RA	KLICKSTEIN LB
RA	PEARSON DT
RA	SH
RA	MARSH HC
RA	CARSON GR

ERN	Sequence
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SL	dhpdqtsfdl1geslctscdpgnvwspaprcq1l1ghcqpahcl1faklktqna
SL	sdfp1gts1kyecrcpvygpf1ccln1wspkdvcrkscktpdpdpmgmhvtid
SL	lvgsr1nyscttphr1l1ghsaecl1sgntahwep1cqr1pc1l1p1t1angdlst
SL	nrenfhysvctvrcmpgsgqkyfelyvgselyctnddqylwspapqcl1pnkctp
SL	pvenqglvsdnralfslnevefrcqpfvmpkprvrcqcalnkwepelpscscvcpd
SL	fmqglngvrlfpvnlqgkavdvceqfqlkgsasycvlagmeslmsvpcvceqif
SL	cpspvlngrhctkclvrfpfkavvrcchodqrdgtsfdl1geslctscdpgnvw
SL	spaprcgl1ghcqpahcl1faklktqnasfpjgrslvscrcpvygpf1ccln1
SL	vsapkrvcrkscktpdpvngmwhv1cd1vgsr1nyscttphr1l1ghsaecl1gn
SL	ahwstckp1cqr1pc1p1t1angdl1stcmthysvrcvrcmpgsgprvrlvge
SL	ps1yctnddqylwspapqcl1pnkctpvenqglvsdnralfslnevefrcqpf
SL	vmkprvrcqcalnkwepelpscscvcpd1p1ngvrl1pvn1q1gkavdvceqf
SL	dlrgasamrctcqqdswspadtevcscdd1mgq1l1ngvrl1pvn1q1gkavdvceqf
SL	q1kgsasycvlagmeslmsvpcvceqf1cpspvl1pnrhngdplvlp1gkavvrc
SL	dhpdqtsfdl1geslctscdpgnvwspaprcq1l1ghcqpahcl1faklktqna
SL	sdfp1gts1kyecrcpvygpf1ccln1wspkdvcrkscktpdpdpmgmhvtid
SL	lvgsr1nyscttphr1l1ghsaecl1sgntahwep1cqr1pc1l1p1t1angdlst
SL	nrenfhysvctvrcmpgsgqkyfelyvgselyctnddqylwspapqcl1pnkctp
SL	pvenqglvsdnralfslnevefrcqpfvmpkprvrcqcalnkwepelpscscvcpd
SL	fmqglngvrlfpvnlqgkavdvceqfqlkgsasycvlagmeslmsvpcvceqif
SL	cpspvlngrhctkclvrfpfkavvrcchodqrdgtsfdl1geslctscdpgnvw
SL	spaprcgl1ghcqpahcl1faklktqnasfpjgrslvscrcpvygpf1ccln1
SL	vsapkrvcrkscktpdpvngmwhv1cd1vgsr1nyscttphr1l1ghsaecl1gn
SL	ahwstckp1cqr1pc1p1t1angdl1stcmthysvrcvrcmpgsgprvrlvge
SL	ps1yctnddqylwspapqcl1pnkctpvenqglvsdnralfslnevefrcqpf
SL	vmkprvrcqcalnkwepelpscscvcpd1p1ngvrl1pvn1q1gkavdvceqf
SL	dlrgasamrctcqqdswspadtevcscdd1mgq1l1ngvrl1pvn1q1gkavdvceqf
SL	q1kgsasycvlagmeslmsvpcvceqf1cpspvl1pnrhngdplvlp1gkavvrc
SL	dhpdqtsfdl1geslctscdpgnvwspaprcq1l1ghcqpahcl1faklktqna
SL	sdfp1gts1kyecrcpvygpf1ccln1wspkdvcrkscktpdpdpmgmhvtid
SL	lvgsr1nyscttphr1l1ghsaecl1sgntahwep1cqr1pc1l1p1t1angdlst
SL	nrenfhysvctvrcmpgsgqkyfelyvgselyctnddqylwspapqcl1pnkctp
SL	pvenqglvsdnralfslnevefrcqpfvmpkprvrcqcalnkwepelpscscvcpd
SL	fmqglngvrlfpvnlqgkavdvceqfqlkgsasycvlagmeslmsvpcvceqif
SL	cpspvlngrhctkclvrfpfkavvrcchodqrdgtsfdl1geslctscdpgnvw
SL	spaprcgl1ghcqpahcl1faklktqnasfpjgrslvscrcpvygpf1ccln1
SL	vsapkrvcrkscktpdpvngmwhv1cd1vgsr1nyscttphr1l1ghsaecl1gn
SL	ahwstckp1cqr1pc1p1t1angdl1stcmthysvrcvrcmpgsgprvrlvge
SL	ps1yctnddqylwspapqcl1pnkctpvenqglvsdnralfslnevefrcqpf
SL	vmkprvrcqcalnkwepelpscscvcpd1p1ngvrl1pvn1q1gkavdvceqf
SL	dlrgasamrctcqqdswspadtevcscdd1mgq1l1ngvrl1pvn1q1gkavdvceqf
SL	q1kgsasycvlagmeslmsvpcvceqf1cpspvl1pnrhngdplvlp1gkavvrc
SL	dhpdqtsfdl1geslctscdpgnvwspaprcq1l1ghcqpahcl1faklktqna
SL	sdfp1gts1kyecrcpvygpf1ccln1wspkdvcrkscktpdpdpmgmhvtid
SL	lvgsr1nyscttphr1l1ghsaecl1sgntahwep1cqr1pc1l1p1t1angdlst
SL	nrenfhysvctvrcmpgsgqkyfelyvgselyctnddqylwspapqcl1pnkctp
SL	pvenqglvsdnralfslnevefrcqpfvmpkprvrcqcalnkwepelpscscvcpd
SL	fmqglngvrlfpvnlqgkavdvceqfqlkgsasycvlagmeslmsvpcvceqif
SL	cpspvlngrhctkclvrfpfkavvrcchodqrdgtsfdl1geslctscdpgnvw
SL	spaprcgl1ghcqpahcl1faklktqnasfpjgrslvscrcpvygpf1ccln1
SL	vsapkrvcrkscktpdpvngmwhv1cd1vgsr1nyscttphr1l1ghsaecl1gn
SL	ahwstckp1cqr1pc1p1t1angdl1stcmthysvrcvrcmpgsgprvrlvge
SL	ps1yctnddqylwspapqcl1pnkctpvenqglvsdnralfslnevefrcqpf
SL	vmkprvrcqcalnkwepelpscscvcpd1p1ngvrl1pvn1q1gkavdvceqf
SL	dlrgasamrctcqqdswspadtevcscdd1mgq1l1ngvrl1pvn1q1gkavdvceqf
SL	q1kgsasycvlagmeslmsv





## BLAST2 Search Results

Sequences Help

Retrieval BLAST2 FASTA ClustalW ICD Assembly PIRIP Translation  
BLAST2 (Hsnu)

Confidential - Property of Incyte Genomics, Inc. SeqServer Version 4.6 Jan 2002

Program: blastp  
Sequence ID(s):☐ 103561CD1 vs. Current: Geneseq\_AA.fasta

NCBI-BLASTP 2.0.10 (Aug-26-1999)

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 103561CD1  
(174 letters)

Database: Current Geneseq\_AA.fasta

1,029,157 sequences; 150,621,602 total letters

Searching.....done

Sequences producing significant alignments:

	Score	E
	(bits)	Value
<input checked="" type="checkbox"/> GSEQ:ABP64720 Human protein SEQ ID 380.	372	e-103
<input checked="" type="checkbox"/> GSEQ:AB68878 Human RECAP polypeptide, SEQ ID NO: 8.	372	e-103
<input checked="" type="checkbox"/> GSEQ:AAW75992 (CM16)-Cys-S-S-(MSMAP-1) polypeptide.	266	6e-71
<input checked="" type="checkbox"/> GSEQ:AAW75991 Complement receptor type 1-like polypeptide CM1	266	6e-71
<input checked="" type="checkbox"/> GSEQ:AAW75990 (CM15)-Cys-S-S-(MSMAP-1) polypeptide.	266	6e-71
<input checked="" type="checkbox"/> GSEQ:AAW75989 Complement receptor type 1-like polypeptide CM1	266	6e-71
<input checked="" type="checkbox"/> GSEQ:ABU11696 Human MDR1 polypeptide SEQ ID 643.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW50797 Human C3B/C4B receptor CR1 (complement receptor	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW441010 Human polypeptide SEQ ID NO 5941.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW39224 Human polypeptide SEQ ID NO 2369.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:ABW11782 Human CR1 protein homologue, SEQ ID NO:2152.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:ABG00287 Novel human diagnostic protein #278.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW5751 Human C3b/C4b receptor (CR1) protein.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW73147 Amino acid sequence of the soluble complement x	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW11810 Human complement type 1 receptor.	256	8e-68
<input checked="" type="checkbox"/> GSEQ:AAW22219 CR1 protein.	256	8e-68

<input checked="" type="checkbox"/> GSEQ:AAW28562 CR1-4 (116K) analogue.	253	7e-67
<input checked="" type="checkbox"/> GSEQ:AAW28552 CR1-4 (78T, 79D) analogue.	252	2e-66
<input checked="" type="checkbox"/> GSEQ:ABW26823 Membrane targeted complement inhibitor peptide.	251	2e-66
<input checked="" type="checkbox"/> GSEQ:ABW26817 Membrane targeted complement inhibitor peptide.	251	2e-66

>GSEQ:ABP64720 Human protein SEQ ID 380.  
Length = 174Score = 372 bits (946), Expect = e-103  
Identities = 174/174 (100%), Positives = 174/174 (100%)

Query: 1 MAPVRLERPPPSRRPFGLLAAVLVLLSFSPOCNVEMLPAPRPTNLTDDEPPIGTY 60  
MAPVRLERPPPSRRPFGLLAAVLVLLSFSPOCNVEMLPAPRPTNLTDDEPPIGTY 60  
Sbjct: 1 MAPVRLERPPPSRRPFGLLAAVLVLLSFSPOCNVEMLPAPRPTNLTDDEPPIGTY 60

Query: 61 LMYECRPGVSGRPFSITICLNSVWTSADKCRKSCNRPDPVNGAHVTKDIOFQSQIK 120  
LMYECRPGVSGRPFSITICLNSVWTSADKCRKSCNRPDPVNGAHVTKDIOFQSQIK 120  
Sbjct: 61 LMYECRPGVSGRPFSITICLNSVWTSADKCRKSCNRPDPVNGAHVTKDIOFQSQIK 120

Query: 121 YSCPRGRLIGSSATCIISGNTVIMDKTPVCDSELYAFLELPHSNFSLE 174  
YSCPRGRLIGSSATCIISGNTVIMDKTPVCDSELYAFLELPHSNFSLE 174  
Sbjct: 121 YSCPRGRLIGSSATCIISGNTVIMDKTPVCDSELYAFLELPHSNFSLE 174

>GSEQ:ABW6878 Human RECAP polypeptide, SEQ ID NO: 8.  
Length = 174Score = 372 bits (946), Expect = e-103  
Identities = 174/174 (100%), Positives = 174/174 (100%)

Query: 1 MAPVRLERPPPSRRPFGLLAAVLVLLSFSPOCNVEMLPAPRPTNLTDDEPPIGTY 60  
MAPVRLERPPPSRRPFGLLAAVLVLLSFSPOCNVEMLPAPRPTNLTDDEPPIGTY 60  
Sbjct: 1 MAPVRLERPPPSRRPFGLLAAVLVLLSFSPOCNVEMLPAPRPTNLTDDEPPIGTY 60

Query: 61 LMYECRPGVSGRPFSITICLNSVWTSADKCRKSCNRPDPVNGAHVTKDIOFQSQIK 120  
LMYECRPGVSGRPFSITICLNSVWTSADKCRKSCNRPDPVNGAHVTKDIOFQSQIK 120  
Sbjct: 61 LMYECRPGVSGRPFSITICLNSVWTSADKCRKSCNRPDPVNGAHVTKDIOFQSQIK 120

Query: 121 YSCPRGRLIGSSATCIISGNTVIMDKTPVCDSELYAFLELPHSNFSLE 174  
YSCPRGRLIGSSATCIISGNTVIMDKTPVCDSELYAFLELPHSNFSLE 174  
Sbjct: 121 YSCPRGRLIGSSATCIISGNTVIMDKTPVCDSELYAFLELPHSNFSLE 174

>GSEQ:AAW75992 (CM16)-Cys-S-S-(MSMAP-1) polypeptide.  
Length = 215Score = 266 bits (674), Expect = 6e-71  
Identities = 120/121 (99%), Positives = 120/121 (99%)

Query: 34 QCNVPEMLPPAPRPTNLTDDEPPIGTYLNTBCRPGVSGRPFSITICLNSVWTSADKCR 93  
QCNVPEMLPPAPRPTNLTDDEPPIGTYLNTBCRPGVSGRPFSITICLNSVWTSADKCR 93  
Sbjct: 2 QCNVPEMLPPAPRPTNLTDDEPPIGTYLNTBCRPGVSGRPFSITICLNSVWTSADKCR 61

Query: 94 KCCNRPDPVNGAHVTKDIOFQSQIKYSCPRGRLIGSSATCIISGNTVIMDKTPVC 153  
KCCNRPDPVNGAHVTKDIOFQSQIKYSCPRGRLIGSSATCIISGNTVIMDKTPVC 153  
Sbjct: 62 KCCNRPDPVNGAHVTKDIOFQSQIKYSCPRGRLIGSSATCIISGNTVIMDKTPVC 121

Query: 154 D 154  
D  
Sbjct: 122 D 122

Score = 40.2 bits (92), Expect = 0.010  
Identities = 38/144 (26%), Positives = 54/144 (37%), Gaps = 23/144 (15%)

Query: 29 SFSFQOC-----NVPEMLPFARPTNLTDPEPIGYLYANECRPGY----SGRPSIIC 78  
+S D+C N P+ P ++ D +F + + Y C GY S II  
Sbjct: 53 TSAKCKRKRKSCRNPPD--PVNGMAHVIKDIQFR--SQIKYSCRGRLIGSSATCIIS 108  
Query: 79 LKNSVTSADKCKRSCRNPPDPVNGMAHYI--KDIQFSQIKYSCRGK-----YRLI 130  
+W + C R C PP NG I + +GS + Y C G + L+  
Sbjct: 109 GNTVIMDNKTPVCDRIICGLPPTIANGDFTSIREYFHGVSVYTHCNLSGRKKVFEIV 168  
Query: 131 GSSSATCIISGNTV--IMDNKTPVC 153  
G S C + V IW P C  
Sbjct: 169 GEPSTYCTSKDQVGWISGPAQC 192

>GSEQ:AAW75991 Complement receptor type 1-like polypeptide CM16/cys.  
Length = 198

Score = 266 bits (674), Expect = 6e-71  
Identities = 120/121 (99%), Positives = 120/121 (99%)

Query: 34 QCNVPEMLPFARPTNLTDPEPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 93  
QCNVPEMLPFARPTNLTDPEPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR  
Sbjct: 2 QCNVPEMLPFARPTNLTDPEPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 61  
Query: 94 KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGRLIGSSATCIISGNTVIMDNKTPVC 153  
KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGRLIGSSATCIISGNTVIMDNKTPVC  
Sbjct: 62 KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGRLIGSSATCIISGNTVIMDNKTPVC 121  
Query: 154 D 154  
D  
Sbjct: 122 D 122

Score = 40.2 bits (92), Expect = 0.010  
Identities = 38/144 (26%), Positives = 54/144 (37%), Gaps = 23/144 (15%)

Query: 29 SFSFQOC-----NVPEMLPFARPTNLTDPEPIGYLYANECRPGY----SGRPSIIC 78  
+S D+C N P+ P ++ D +F + + Y C GY S II  
Sbjct: 53 TSAKCKRKRKSCRNPPD--PVNGMAHVIKDIQFR--SQIKYSCRGRLIGSSATCIIS 108  
Query: 79 LKNSVTSADKCKRSCRNPPDPVNGMAHYI--KDIQFSQIKYSCRGK-----YRLI 130  
+W + C R C PP NG I + +GS + Y C G + L+  
Sbjct: 109 GNTVIMDNKTPVCDRIICGLPPTIANGDFTSIREYFHGVSVYTHCNLSGRKKVFEIV 168  
Query: 131 GSSSATCIISGNTV--IMDNKTPVC 153  
G S C + V IW P C  
Sbjct: 169 GEPSTYCTSKDQVGWISGPAQC 192

>GSEQ:AAW75990 (CM15)-Cys-S-S-(MSMAP-1) polypeptide.  
Length = 215

Score = 266 bits (674), Expect = 6e-71  
Identities = 120/121 (99%), Positives = 120/121 (99%)

Query: 34 QCNVPEMLPFARPTNLTDPEPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 93  
QCNVPEMLPFARPTNLTDPEPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR  
Sbjct: 2 QCNVPEMLPFARPTNLTDPEPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 61  
Query: 94 KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGRLIGSSATCIISGNTVIMDNKTPVC 153  
KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGRLIGSSATCIISGNTVIMDNKTPVC  
Sbjct: 62 KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGRLIGSSATCIISGNTVIMDNKTPVC 121  
Query: 154 D 154  
D

Sbjct: 122 D 122

Score = 39.9 bits (91), Expect = 0.013  
Identities = 38/144 (26%), Positives = 54/144 (37%), Gaps = 23/144 (15%)

Query: 29 SFSFQOC-----NVPEMLPFARPTNLTDPEPIGYLYANECRPGY----SGRPSIIC 78  
+S D+C N P+ P ++ D +F + + Y C GY S II  
Sbjct: 53 TSAKCKRKRKSCRNPPD--PVNGMAHVIKDIQFR--SQIKYSCRGRLIGSSATCIIS 108  
Query: 79 LKNSVTSADKCKRSCRNPPDPVNGMAHYI--KDIQFSQIKYSCRGK-----YRLI 130  
+W + C R C PP NG I + +GS + Y C G + L+  
Sbjct: 109 GNTVIMDNKTPVCDRIICGLPPTIANGDFTSIREYFHGVSVYTHCNLSGRKKVFEIV 168  
Query: 131 GSSSATCIISGNTV--IMDNKTPVC 153  
G S C + V IW P C  
Sbjct: 169 GEPSTYCTSKDQVGWISGPAQC 192

>GSEQ:AAW75989 Complement receptor type 1-like polypeptide CM15/cys.  
Length = 198

Score = 266 bits (674), Expect = 6e-71  
Identities = 120/121 (99%), Positives = 120/121 (99%)

Query: 34 QCNVPEMLPFARPTNLTDPEPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 93  
QCNVPEMLPFARPTNLTDPEPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR  
Sbjct: 2 QCNVPEMLPFARPTNLTDPEPIGYLYANECRPGYSGRPSIICLKNSVTSADKCKR 61  
Query: 94 KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGRLIGSSATCIISGNTVIMDNKTPVC 153  
KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGRLIGSSATCIISGNTVIMDNKTPVC  
Sbjct: 62 KSCRNPDPVNGMAHYIKDIQFSQIKYSCRGRLIGSSATCIISGNTVIMDNKTPVC 121  
Query: 154 D 154  
D  
Sbjct: 122 D 122

Score = 39.9 bits (91), Expect = 0.013  
Identities = 38/144 (26%), Positives = 54/144 (37%), Gaps = 23/144 (15%)

Query: 29 SFSFQOC-----NVPEMLPFARPTNLTDPEPIGYLYANECRPGY----SGRPSIIC 78  
+S D+C N P+ P ++ D +F + + Y C GY S II  
Sbjct: 53 TSAKCKRKRKSCRNPPD--PVNGMAHVIKDIQFR--SQIKYSCRGRLIGSSATCIIS 108  
Query: 79 LKNSVTSADKCKRSCRNPPDPVNGMAHYI--KDIQFSQIKYSCRGK-----YRLI 130  
+W + C R C PP NG I + +GS + Y C G + L+  
Sbjct: 109 GNTVIMDNKTPVCDRIICGLPPTIANGDFTSIREYFHGVSVYTHCNLSGRKKVFEIV 168  
Query: 131 GSSSATCIISGNTV--IMDNKTPVC 153  
G S C + V IW P C  
Sbjct: 169 GEPSTYCTSKDQVGWISGPAQC 192

>GSEQ:ABU11696 Human MDP1 polypeptide SEQ ID 643.  
Length = 2044

Score = 256 bits (647), Expect = 8e-68  
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLAALVLLSFS--DQCNVPEMLPFARPTNLTDPEPIGYLYANECRPGYSGRPSI 76  
G LLA +VLL + QCN PEMLPFARPTNLTDPEPIGYLYANECRPGYSGRPSI  
Sbjct: 30 GSLLAIVVLLALPVAMQCNAPBMLPFARPTNLTDPEPIGYLYANECRPGYSGRPSI 89  
Query: 77 ICLKNSVTSADKCKRSCRNPPDPVNGMAHYIKDIQFSQIKYSCRGRLIGSSAT 136

Query: 90 ICLNSWMT ARD-C-RKSCRPDPVNGM HVIK I0FSGQIKYSC KGRILIGSSSAT  
Sbjct: 137 CIIAGTVMIDNKTPTCD 154  
Query: 137 CIIAGTVMIDNKTPTCD 154  
Sbjct: 150 CIIAGTVMIDNKTPTCD 167

Score = 176 bits (442), Expect = 9e-44  
Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSFSIDQCNVPEMLPFARPTNLTDDEFPPIGTLYANECRPGYSGR-PFSITICLNKSWTS 87  
Sbjct: 1394 LSTRAGHKTPEOPFPASFTPIINDEFPVGSILNECRPGYSGRPGFSGMPTSLCLENLWSSV 1453  
Query: 88 KDKCRKSCRNPPDPVNGMAHVIKDIOFSGQIKYSCPKGYRLIGSSSANCIIISGNVTIYMD 147  
Sbjct: 1454 EDNCRKSCGPEPEPNMGVHINTDQFSGTVNYSNMGFRILIGSPTCLVSGNVTIYMD 1513  
Query: 148 NKTPTVCD 154  
Sbjct: 1514 KKAPECE 1520

Score = 166 bits (417), Expect = 8e-41  
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 CNVPEMLPFARPTNLTDDEFPPIGTLYANECRPGYSGR-PFSITICLNKSWTSADKCKRK 94  
Sbjct: 948 COAPDHPLFAKLTQTNASDPIGTSLKYECPREYGRPPTICLDNLVWSPKDVCKRK 1007  
Query: 95 SCNRPDPVNGMAHVIKDIOFSGQIKYSCPKGYRLIGSSSANCIIISGNVTIYMDKTPVC 153  
Sbjct: 1008 SCKTPEPDPVNGMAHVITDIOGSRINYSCTGTHLIGHSSAECILSGMAHNSKTPPIC 1066

Score = 164 bits (412), Expect = 3e-40  
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVPEMLPFARPTNLTDDEFPPIGTLYANECRPGYSGR-PFSITICLNKSWTSADKCKRK 94  
Sbjct: 498 COAPDHPLFAKLTQTNASDPIGTSLKYECPREYGRPPTICLDNLVWSPKDVCKRK 557  
Query: 95 SCNRPDPVNGMAHVIKDIOFSGQIKYSCPKGYRLIGSSSANCIIISGNVTIYMDKTPVC 153  
Sbjct: 558 SCKTPEPDPVNGMAHVITDIOGSRINYSCTGTHLIGHSSAECILSGMAHNSKTPPIC 616

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFSIDQCNVPEMLPFARPTNLTDDEFPPIGTLYANECRPGYSGR-PFSITICLNKSWTS 86  
Sbjct: 745 LPSGSRVCPPEPDLHAERTQKRD-NFSPQEVFYSCEBGVDLAGAASNRCTPGQWSP 803  
Query: 87 AKDKCRKSCRNPPDPVNGMAHVIKDIOFSGQIKYSCPKGYRLIGSSSANCIIISGNVTI 145  
Sbjct: 804 AALPCEVYKSCDDPFGQLNGRVLPVNLQGLAKVDPCDEGQLKGSASVYLAGMESTL 863  
Query: 146 WDNKTPVCD 154  
Sbjct: 864 WNSVPECE 872

Score = 68.7 bits (165), Expect = 3e-11

Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFSIDQCNVPEMLPFARPTNLTDDEFPPIGTLYANECRPGYSGR-PFSITICLNKSWTS 86  
Sbjct: 295 LPSGSRVCPPEPDLHAERTQKRD-NFSPQEVFYSCEBGVDLAGAASNRCTPGQWSP 353  
Query: 87 AKDKCRKSCRNPPDPVNGMAHVIKDIOFSGQIKYSCPKGYRLIGSSSANCIIISGNVTI 145  
Sbjct: 354 AALPCEVYKSCDDPFGQLNGRVLPVNLQGLAKVDPCDEGQLKGSASVYLAGMESTL 413  
Query: 146 WDNKTPVCD 154  
Sbjct: 414 WNSVPECE 422

Score = 64.8 bits (155), Expect = 4e-10  
Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)

Query: 28 LSSFSIDQCNVPEMLPFARPTNLTDDEFPPIGTLYANECRPGYSGR-PFSITICLNKSWTS 86  
Sbjct: 1195 LPSGSRVCPPEPDLHAERTQKRD-NFSPQEVFYSCEBGVDLAGAASNRCTPGQWSP 1253  
Query: 87 AKDKCRKSCRNPPDPV-NGMAHVIKDIOFSGQIKYSCPKGYRLIGSSSANCIIISGNVTI 145  
Sbjct: 1254 EAPRCVAYSCDDPDLQPLPHGRVLPVNLQGLAKVSPVCDGFRILIGSVSHCVLWGRSL 1313  
Query: 146 WDNKTPVCD 154  
Sbjct: 1314 WNSVPECE 1322

Score = 61.3 bits (146), Expect = 5e-09  
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 LNDDEFPPIGTLYANECRPGYSGR-PFSITICLNKSWTSADKCKRKSCRNPPDV-NGM 106  
Sbjct: 1668 LSHODNFSQOEYFYSCEPSYDLRGAASLHCTPGQWSPKACTVKSDDPDLQPLPHGR 1727  
Query: 107 AHVINDIOFSGQIKYSCPKGYRLIGSSSANCIIISGNVTIYMDKTPVC 154  
Sbjct: 1728 VILLPLNLQGLAKVSPVCDGFRILIGSVSHCVLWGRSLVPECE 1775

Score = 48.0 bits (112), Expect = 5e-05  
Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)

Query: 26 LLSFSIDQCNV---PEMLPFARPTNLTDDEFPPIGTLYANECRPGYSGR-PFSITICL 79  
Sbjct: 1448 LVMSSVDECRKSCGPEPEPNMGVHINTDQF-GSTVYSCNGBRLIGSP-STCTL 1504  
Query: 80 ---KNSVTSADKCKRKSCRNPPDPVNGMAHVIKDIOF--GSOIYSCPPG-----YR 128  
Sbjct: 1505 VSGNNVYMDKAPICELIISCEPPTISNGDFYNNRTFPHNGVTVYTCCHGPDGQLPE 1564  
Query: 129 LIGSSSANCIIISGNVTI-INDKTPVCDSEIK 158  
Sbjct: 1565 LVGERSTVCTSKDDQVWSSPPRCISTYRK 1595

Score = 46.5 bits (108), Expect = 1e-04  
Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)

Query: 57 IGVTLNTECRPGY--SGRPPS--IICLNKSWTSADKCKRKSCRNPPDPVNG--NAHYI 110  
Sbjct: 1736 LGAKVSPVCDGFRILIGSVSHCVLWGRSLVPECEQDIFCRFPAIILNGHRTPE 1795

Query: 111 KDIOFSGQIKYSCP-----KGYRLIGSSSACII--SGNTVIMDKTPVC 154  
DI +G +I Y+C + LIG SS C GN V W + P C+  
Sbjct: 1796 GDIPYKKEISYACDHPHRCMTPLIGSSIRCTSDPQNGV-MSPAPRC 1846

Score = 43.8 bits (101), Expect = 9e-04  
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTVLANECPRGY----SGRPSTICLKNVWTSADKCKRSCNPPDPVNG--MAHYIK 111  
G +Y C GY S II +W+ C R C PP NG ++ +  
Sbjct: 129 GSGIKYSCCKGRLIGSSSACIIISGDTVIMDEPPICDRIPOGLPPTINGISTNE 188

Query: 112 DIOGSGQIKYSCP-----YRLIGSSSACIIISGNTVIMDKTPVC 153  
+GS +Y C G +L+G S C + + V IW P C  
Sbjct: 189 NFHIGSVVTRCNFSGGRKRVELVGEPSICTSDNDQVIGMGPAPC 237

Score = 43.0 bits (99), Expect = 0.002  
Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)

Query: 58 GTVLANECPRGY--GRPSIICLKNVWTSADKCKRSCNPPDPVNGMAHYI--KD 112  
G +Y C PGY G+ F I C +W+ CR +C P +NG++ + K  
Sbjct: 1875 GMTISYICDPGYLLVKGKF-IFCTDQIWSQLDHYCKEVNCFPLF-MNGISKELEMKV 1932

Query: 113 IQGSGQIKYSCPRGRLIGSSSACIIISGNTVIMDKTPVCSEKVAFL 162  
+G + C GY L GS + C S A +  
Sbjct: 1933 YHFGDVYTLKCEDFTLIGSPISQCADDR--WDPLACTSRHMDLI 1979

Score = 43.0 bits (99), Expect = 0.002  
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTVLANECPRGYS--GRPSIICLKNV--WTSADKCKRSCNPPDPVNG--MA 107  
+ +G+ +NY C G+ G + L + W++ C+R C PP NG ++  
Sbjct: 575 DVOGSRINVSCTGHRILIGSSACIIISGNTVIMDKTPVCSEKVAFL 634

Query: 108 HVHIDIOFSGQIKYSCP-----YRLIGSSSACIIISGNTVIMDKTPVC 153  
++ +GS +Y C G +L+G S C + + V IW P C  
Sbjct: 635 TTRNFHIGSVVTRCNFSGGRKRVELVGEPSICTSDNDQVIGMGPAPC 687

Score = 43.0 bits (99), Expect = 0.002  
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGTVLANECPRGY----SGRPSTICLKNVWTSADKCKRSCNPPDPVNG--MAHYI 110  
+G +++ C G+ S ++ S+W ++ C+ C NP +NG  
Sbjct: 1283 LGANVSFVCDGDFRLKGSASVHCVALGMRSLMNSVPVCEHICPPALINRHTGPS 1342

Query: 111 KDIOFSGQIKYSCP-----KGYRLIGSSSACIIISGNTVIMDKTPVCSEKVAFL 158  
DI +G +I Y+C + LIG SS C GN V W + P C+ ++  
Sbjct: 1343 GDIPYKKEISYACDHPHRCMTPLIGSSIRCTSDPQNGV-MSPAPRCSELR 1397

Score = 42.6 bits (98), Expect = 0.002  
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTVLANECPRGYSGRPSI--IICLKNVWTSADKCKRSCNPPDPVNG--MA 107  
+ +G+ +NY C G+ S I+ + W++ C+R C PP NG ++  
Sbjct: 1023 DVOGSRINVSCTGHRILIGSSACIIISGNTVIMDKTPVCSEKVAFL 1084

Query: 108 HVHIDIOFSGQIKYSCP-----YRLIGSSSACIIISGNTVIMDKTPVC 153  
++ +GS +Y C G +L+G S C + + V IW P C  
Sbjct: 1085 TTRNFHIGSVVTRCNFSGGRKRVELVGEPSICTSDNDQVIGMGPAPC 1137

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTVLANECPRGY----SGRPSTICLKNVWTSADKCKRSCNPPDPVNGMAHYIKD 112  
+G +++ C G+ S ++ S+W S+ C++ C +PP NG H K  
Sbjct: 383 LGANVDFVCDGDFRLKGSASVHCVALGMRSLMNSVPVCEHICPPALINRHTGPS 441

Query: 113 IQ--FGSQIKYSCP-----KGYRLIGSSSACII--SGNTVIMDKTPVC 153  
++ FG +Y+C +LIG S+ C GN V W + P C  
Sbjct: 442 LEVFPFGKAVNTCDHPHRCMTPLIGSSIRCTSDPQNGV-MSPAPRC 492

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTVLANECPRGY----SGRPSTICLKNVWTSADKCKRSCNPPDPVNGMAHYIKD 112  
+G +++ C G+ S ++ S+W S+ C++ C +PP NG H K  
Sbjct: 833 LGANVDFVCDGDFRLKGSASVHCVALGMRSLMNSVPVCEHICPPALINRHTGPS 891

Query: 113 IQ--FGSQIKYSCP-----KGYRLIGSSSACII--SGNTVIMDKTPVC 153  
++ FG +Y+C +LIG S+ C GN V W + P C  
Sbjct: 892 LEVFPFGKAVNTCDHPHRCMTPLIGSSIRCTSDPQNGV-MSPAPRC 942

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPAPRPNLMDP-----EPIGTVLANECPRGYSGRPF-----SIIICLKN-- 81  
+P LP PT DF F G+ +Y C PG GR SI C N  
Sbjct: 619 IPCLP--PTIANGDFISTNNEHFGSVVTRCNFSGGRKRVELVGEPSICTSDND 675

Query: 82 --SWTSADKCKRSCNPPDPVNGMAHYID----IQGSGQIKYSCPRGRLIGSSSA 135  
+W+ +C + PP+ NG+ ++ D +++ C G+ + G  
Sbjct: 676 QVWISGAPAOQIIPNCTPVENGEI--LVSDNLSLFLSINEVFERQDGFVAKGPRV 733

Query: 136 TCIIISGNTVIMDKTPVC 153  
C W+ + P C  
Sbjct: 734 KQALNK--WEPELPSC 748

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPAPRPNLMDP-----EPIGTVLANECPRGYSGRPF-----SIIICLKN-- 81  
+P LP PT DF F G+ +Y C PG GR SI C N  
Sbjct: 169 IPCLP--PTIANGDFISTNNEHFGSVVTRCNFSGGRKRVELVGEPSICTSDND 225

Query: 82 --SWTSADKCKRSCNPPDPVNGMAHYID----IQGSGQIKYSCPRGRLIGSSSA 135  
+W+ +C + PP+ NG+ ++ D +++ C G+ + G  
Sbjct: 226 QVWISGAPAOQIIPNCTPVENGEI--LVSDNLSLFLSINEVFERQDGFVAKGPRV 283

Query: 136 TCIIISGNTVIMDKTPVC 153  
C W+ + P C  
Sbjct: 284 KQALNK--WEPELPSC 298

Score = 36.4 bits (82), Expect = 0.15  
Identities = 33/117 (28%), Positives = 45/117 (38%), Gaps = 21/117 (17%)

Query: 54 EPIGTVLANECPRGYS--GRPSI--CLK--NSWTSADKCKR--SCRNP 99  
+ P G +Y+Y C G F++I C N W+S C++ +C +P  
Sbjct: 1797 DIPYKKEISYACDHPHRCMTPLIGSSIRCTSDPQNGVMSAPRCSELR 1856

Query: 100 PDPVNGM--AHVTKDIOFSGQIKYSCPRGRLIGSSSACIIISGNTVIMDKTPVC 153



Query: 1857 P NG HV + G I Y C GY L+G C G IW C  
Sbjct: 1857 P K I Q N G H Y I G N V S L Y L P - G M T I S Y I C D P R G L V L A K G I R F C T O G --- I N S Q L D H Y C 1909

Score = 36.4 bits (82), Expect = 0.15  
Identities = 33/128 (25%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 P N I L T D P F --- E F P I G T A L Y E C R P G Y S G R P F --- S I I C L A K N --- S W T S A K 88  
P F D F P G F + Y + C G G S I C W M + S

Sbjct: 1528 P T I S G D F Y S N N R K T S F N G T V T V Y Q C H T G D G S Q L F E L V G R S I Y C T S K D Q V G W S S P 1587

Query: 89 D K C R K R S C N P D P V N G M A H V I K D I Q F G S Q --- I K I S C P K Y I L I S S A C I I S G N T V I 145  
+ C + P + N + V + F S + + + C G + + S + C + G

Sbjct: 1588 P H C I S T K C T A P E V E N A I - R V P E N S F P S L T E I V R F C Q P E F V A G S H T V C C T N R --- 1643

Query: 146 W D N K T P V C 153  
W K P C

Sbjct: 1644 W G F K L P H C 1651

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 C N V E M L P F A R P N L T D D F E P I G T A L Y E C R P G Y S - G R P S I I --- C L K --- N S V 83  
C P + P R T + P P G + N Y C P G F + I C N V

Sbjct: 426 C P S P P I T N G H N G K P L E V - P P E K T V N Y T C D P H D R G T S F D L I G E T I C T S D P O G N V 484

Query: 84 W T S A K D K C - R K S C R N P D P V N G M A H V --- I K D I Q F G S Q I K Y S C P K Y I L I S S A C I I 139  
W + S + C C + P + D G + K Y C Y S T C +

Sbjct: 485 W S S P A P R C G I L H C Q A P D H P L F A L K I Q T N A S D P I G T S I A K Y E C R P E Y - Y G R P S I C L - 542

Query: 140 S G N T V I W D N K T P V C 153  
+ + + W + V C

Sbjct: 543 - - D N L W S S P K D V C 554

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 C N V E M L P F A R P N L T D D F E P I G T A L Y E C R P G Y S - G R P S I I --- C L K --- N S V 83  
C P + P R T + P P G + N Y C P G F + I C N V

Sbjct: 876 C P S P P I T N G H N G K P L E V - P P E K A V N Y T C D P H D R G T S F D L I G E T I C T S D P O G N V 934

Query: 84 W T S A K D K C - R K S C R N P D P V N G M A H V --- I K D I Q F G S Q I K Y S C P K Y I L I S S A C I I 139  
W + S + C C + P + D G + K Y C Y S T C +

Sbjct: 935 W S S P A P R C G I L H C Q A P D H P L F A L K I Q T N A S D P I G T S I A K Y E C R P E Y - Y G R P S I C L - 992

Query: 140 S G N T V I W D N K T P V C 153  
+ + + W + V C

Sbjct: 993 - - D N L W S S P K D V C 1004

>GSE01AAN50797 Human C3B/C4B receptor CRL (complement receptor type 1).

Length = 2039

Score = 256 bits (647), Expect = 8e-68  
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 G I L L A A L I L L S S F S - D O C N P E M L P F A R P N L T D D F E P I G T A L Y E C R P G Y S G R P S I 76  
G I L A + I L L + O C N P E M L P F A R P N L T D D F E P I G T A L Y E C R P G Y S G R P S I

Sbjct: 25 G S I L A V V I L L A L P V A M G C N A P E M L P F A R P N L T D D F E P I G T A L Y E C R P G Y S G R P S I 84

Query: 77 I C L K N S V T A K D C R K S C N P D P V N G M A H V I K D I Q F G S Q I K Y S C P K Y I L I S S A C I I 136  
I C L K N S V T A K D + C + R K S C N P D P V N G M H V I K I Q F G S Q I K Y S C K Y R L I G S S A T

Sbjct: 85 I C L K N S V T A K D C R K S C N P D P V N G M A H V I K D I Q F G S Q I K Y S C T G Y R L I G S S A T 144

Query: 137 C I I S G T V I W D N K T P V C 154  
C I I S G + T V I W D N + T P + C D

Sbjct: 145 C I I S G T V I W D N K T P V C 162

Score = 176 bits (442), Expect = 9e-44  
Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 I S S F S D C N V P E M L P F A R P N L T D D F E P I G T A L Y E C R P G Y S G R P S I I C L K N S V T A K D C R K 87  
I S + C P E P F A P P + D F E P + C T L Y E C R P G Y S G R P S I I C L N W M + S

Sbjct: 1389 I S V A G H C T P E Q P F P A S P T I P I N D F E P I G T A L Y E C R P G Y S G R P S I I C L N W M S S P 1448

Query: 88 K D C R K R S C N P D P V N G M A H V I K D I Q F G S Q I K Y S C P K Y I L I S S A C I I S G N T V I W D 147  
+ D C + R K S C P P + P N G M H + D Q F G S + Y S C + G + R L I G S S T C + + S G N V W D

Sbjct: 1449 E D N C R R S C G P E P F N G M A H V I N T D I Q F G S T V S C N G E R L I G S P T T C L V A G N N V T W D 1508

Query: 148 N K T P V C 154  
K P C +

Sbjct: 1509 K K A P I C E 1515

Score = 166 bits (417), Expect = 8e-41  
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 C N V E M L P F A R P N L T D D F E P I G T A L Y E C R P G Y S G R P S I I C L K N S V T A K D C R K 94  
C P + P A + T + P P I G T L Y E C R P Y G R P S I C L N W M + S K D C R K

Sbjct: 943 C Q A P D H P L F A L K I Q T N A S D P I G T S I A K Y E C R P E Y G R P S I C L N L W S S P K D V C R K 1002

Query: 95 S C R N P D P V N G M A H V I K D I Q F G S Q I K Y S C P K Y I L I S S A C I I S G N T V I W D N K T P V C 153  
S C + P D P V N G M H V I D I Q G S + I Y S C G + R L I G S S A C I + S G N T W K P + C

Sbjct: 1003 S C K T P D P V N G M A H V I T D I Q G S R I N Y S C T G H R L I G H S S A C I I S G N T A M S T K P P I C 1061

Score = 164 bits (412), Expect = 3e-40  
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 C N V E M L P F A R P N L T D D F E P I G T A L Y E C R P G Y S G R P S I I C L K N S V T A K D C R K 94  
C P + P A + T + P P I G T L Y E C R P Y G R P S I C L N W M + S K D C R K

Sbjct: 493 C Q A P D H P L F A L K I Q T N A S D P I G T S I A K Y E C R P E Y G R P S I C L N L W S S P K D V C R K 552

Query: 95 S C R N P D P V N G M A H V I K D I Q F G S Q I K Y S C P K Y I L I S S A C I I S G N T V I W D N K T P V C 153  
S C + P D P V N G M H V I D I Q G S + I Y S C G + R L I G S S A C I + S G N T W K P + C

Sbjct: 553 S C K T P D P V N G M A H V I T D I Q G S R I N Y S C T G H R L I G H S S A C I I S G N A M S T K P P I C 611

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 L S S F S D C N V P E M L P F A R P N L T D D F E P I G T A L Y E C R P G Y S G R - P F S I I C L K N S V T A K D C R K 86  
L S S C C P + A T D P G + Y C R O Y R S + C W +

Sbjct: 740 L F S C S N V C O P P D V L H A R T O R D E - N F S P Q E V F Y S C P G I D R G A S M R C T P O G M S P 798

Query: 87 A K D C R K S C R N - P D P V N G M A H V I K D I Q F G S Q I K Y S C P K Y I L I S S A C I I S G N T V I 145  
A C + K S C + N G + + Q G + + + C + G + + L G S S + C + + G +

Sbjct: 799 A A P T C E V S C D E W Q L I N G R V L P V N L Q L A K A V D F C D E G O L K G S S A S Y C V L A G E S L 858

Query: 146 W D N K T P V C 154  
W + + P V C +

Sbjct: 859 W N S S V P C E 867

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFSDDCNVPEMLPFARPTNLTDPEPIGTATNECRPGYSGR--PFSIICLNKNSWTS 86  
L S S C P + A T D P G + Y C PGY R S+ C W+  
Sbjct: 290 LPSCSNVCOPEPVLHARTORD--NFSPOEVYFSCPEPDLRGASLRCTPGQMSF 348

Query: 87 AKDKCKRSKRN--PDPVNGAHVTKIDQFSGQIKYSCPKGYRLIGSSANCIISGNTV 145  
A C KSC + +NG +Q G+++ + C +G++L GSS+ C++ G +  
Sbjct: 349 AATPEKWSGDDPMGQLNGRVLEPVNLQLAHVPCDEGQKSSASVYLAAGNESL 408

Query: 146 MNKTPVCD 154  
W+ FVC+  
Sbjct: 409 WNSVFPCE 417

Score = 64.8 bits (155), Expect = 4e-10  
Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)

Query: 28 LSSFSDDCNVPEMLPFARPTNLTDPEPIGTATNECRPGYSGR--PFSIICLNKNSWTS 86  
L S S C P + T D P G + Y C PGY R S+ C W+  
Sbjct: 1190 LPSCSNVCOPEPVLHARTORD--NFSPOEVYFSCPEPDLRGASLRCTPGQMSF 1248

Query: 87 AKDKCKRSKRN--PDPVNGAHVTKIDQFSGQIKYSCPKGYRLIGSSANCIISGNTV 145  
+ C KSC + +G +Q G+++ + C +G++L GSS + C++ G +  
Sbjct: 1249 EAPFCAYKSCDPLGOLPHGRVLPFLNLQGAHVSPVCDGRLKSSSVSHCVLWGMSL 1308

Query: 146 MNKTPVCD 154  
W+N PVC+  
Sbjct: 1309 WNSVFPCE 1317

Score = 61.3 bits (146), Expect = 5e-09  
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 LTDPEPIGTATNECRPGYSGR--PFSIICLNKNSWTSADKCKRSKRNPDVNG--NQM 106  
L+ P G + Y C P Y R S+ C W+ +C KSC + +G  
Sbjct: 1663 LSHDNVSPQEVFSCPEPDLRGASLRCTPGQMSFEPALQOLPHGR 1722

Query: 107 AHVTKIDQFSGQIKYSCPKGYRLIGSSANCIISGNTVIMDNKTPVCD 154  
+ +Q G+++ + C +G+L G S++ C++G +W++ PVC+  
Sbjct: 1723 VILPLNLQGAHVSPVCDGRLKRSASHCVLAAGKALMNSVFPCE 1770

Score = 48.0 bits (112), Expect = 5e-05  
Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)

Query: 26 LLSFSDDCNV---PEMLPFARPTNLTDPEPIGTATNECRPGYSGR--PFSIICL 79  
L+ S S D C P P F P ++ D +F G+ +NY C G+ G P S CL  
Sbjct: 1443 LMSVSEVDCNRKRSKCGPPEPFGNVAHINTDQF--GSTVNSCNGFRLLGSP--STCCL 1499

Query: 80 ---KNSVWTSADKCKRSKRNPDVNGAHVTKIDQF--GSOIKYSCPKG-----YR 128  
N W M C+ SC PP NG + F G+ + Y C G +  
Sbjct: 1500 VSGNNTWMDKAPICETIISCEPPTISNGDPYISNNRISFHHGVVYTCGHDGQGLFE 1559

Query: 129 LIGSSANCIISGNTV--IMDNKTPVCDSELK 158  
L+G S C + V W+ + P C S K  
Sbjct: 1560 LVGRSITCTSKDQVGVWSSPPEICISTWK 1590

Score = 46.5 bits (108), Expect = 1e-04  
Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)

Query: 57 IGTATNECRPGY--SGRPFSS--ITCLAKNSWTSADKCKRSKRNPDVNG--MAHVI 110  
+G + +C G+ GR S + + +W S+ C++ C NPP +NG  
Sbjct: 1731 LGATVSPVCDGFRKGRSASHCVLAAGKALMNSVFPVCIQCPFPALLNGRHTGPF 1790

Query: 111 KDQFSGQIKYSCP-----KGYRLIGSSANCIIS--SGNTVIMDNKTPVCD 154  
DI +G +I Y+C + LIG SS C GN V W + P C +  
Sbjct: 1791 GDIPYGEISYACDTHPDGKMTFNLIGESIRCTSDQGNV--WSSPAFCE 1841

Score = 43.8 bits (101), Expect = 9e-04  
Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)

Query: 58 GTYLNEYCRPGY--SGRPFSSITCLAKNSWTSADKCKRSKRNPDVNG--MAHVI 111  
G + +Y C PGY G+ F I C +W+ CK +C P +N++ + K  
Sbjct: 1870 GATISTYCDPGLVWKGFR--IFCDQGISQDHYCKEAVNCSPFL--MNGISELEMKV 1927

Query: 113 IQFSGQIKYSCPKGYRLIGSSANCIISGNTVIMDNKTPVCDSELK 162  
+G + C GY L GS + C WD C S A +  
Sbjct: 1928 YHGDVYTLKCEDGYTLGSPWSCQADR--MDPLACTSRADHALLI 1974

Score = 43.8 bits (101), Expect = 9e-04  
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTYLNEYCRPGY--SGRPFSSITCLAKNSWTSADKCKRSKRNPDVNG--MAHVI 111  
G+ + Y C GY S II +W+ C R C PP NG ++ +  
Sbjct: 124 GSOIKYSCPKGYRLIGSSANCIISGNTVIMDNKTPVCDIPGLPPTTGDPISITNRE 183

Query: 112 DIQFSGQIKYSCPKG-----YRLIGSSANCIISGNTV--IMDNKTPVCD 153  
+ +GS + Y C G +L+G S C + + V IW P C  
Sbjct: 184 NFHGSVVTYRCNPGSGGRVPELVGEPSTYCTSDNDQVIGMSGAPQC 232

Score = 43.0 bits (99), Expect = 0.002  
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTATNECRPGYSGR--PFSIICLNKNSV--WTSADKCKRSKRNPDVNG--NA 107  
+ +G+ +NY C G+ G + L + W++ C+R C PP NG ++  
Sbjct: 570 DIOVGSINISCTGHRLLIGSSANCIISGNAHMSSTPFCORICGLPPTIANGDFTS 629

Query: 108 HVTKIDQFSGQIKYSCPKG-----YRLIGSSANCIISGNTV--IMDNKTPVCD 153  
++ +GS + Y C G +L+G S C + + V IW P C  
Sbjct: 630 TNRNHFHGSVVTYRCNPGSGGRVPELVGEPSTYCTSDNDQVIGMSGAPQC 682

Score = 43.0 bits (99), Expect = 0.002  
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGTATNECRPGYSGRPFSSITCLAKNSWTSADKCKRSKRNPDVNG--MAHVI 110  
+G + +C G+ S ++ S+W ++ C+ C NPP +NG  
Sbjct: 1278 LGATVSPVCDGFRKGRSASHCVLAAGKALMNSVFPVCIQCPFPALLNGRHTGPF 1337

Query: 111 KDQFSGQIKYSCP-----KGYRLIGSSANCIIS--SGNTVIMDNKTPVCDSELK 158  
DI +G +I Y+C + LIG S+ C GN V W + P C+ ++  
Sbjct: 1338 GDIPYGEISYACDTHPDGKMTFNLIGESTICTSDPHNGV--WSSPAFCELSVR 1392

Score = 42.6 bits (98), Expect = 0.002  
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTATNECRPGYSGRPFSSITCLAKNSWTSADKCKRSKRNPDVNG--MA 107  
+G+ +NY C G+ S I+ + W++ C+R C PP NG ++  
Sbjct: 1020 DIOVGSINISCTGHRLLIGSSANCIISGNAHMSSTPFCORICGLPPTIANGDFTS 1079

Query: 108 HVTKIDQFSGQIKYSCPKG-----YRLIGSSANCIISGNTV--IMDNKTPVCD 153  
++ +GS + Y C G +L+G S C + + V IW P C  
Sbjct: 1080 TNRNHFHGSVVTYRCNPGSGGRVPELVGEPSTYCTSDNDQVIGMSGAPQC 1132

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTLYANECRPGY-----SGRPSIICLNKSWTSADKCRKSCRNPPDPVNGMAHVIKD 112  
+G +++ C G+ S +++ S+W S+ C++ C +PP NG H K  
Sbjct: 378 LGAKVDVCDGDFQKGSASVYCVLAGESLMWSSVPCQIICPSPPVPIING-RRTGKP 436

Query: 113 IQ---FGSQIKYSCP-----KGYRLIGSSSANCII--SGNTVIMDNKTTPVC 153  
++ FG + Y+C + LIG S+ C GN V W + P C  
Sbjct: 437 LEVFPFGKAVNYTCDPHDRGTSFDLIGESTRICTSDPQNGV-WSPAPRC 487

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTLYANECRPGY-----SGRPSIICLNKSWTSADKCRKSCRNPPDPVNGMAHVIKD 112  
+G +++ C G+ S +++ S+W S+ C++ C +PP NG H K  
Sbjct: 828 LGAKVDVCDGDFQKGSASVYCVLAGESLMWSSVPCQIICPSPPVPIING-RRTGKP 886

Query: 113 IQ---FGSQIKYSCP-----KGYRLIGSSSANCII--SGNTVIMDNKTTPVC 153  
++ FG + Y+C + LIG S+ C GN V W + P C  
Sbjct: 887 LEVFPFGKAVNYTCDPHDRGTSFDLIGESTRICTSDPQNGV-WSPAPRC 937

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFPAPFNLTDDP-----EPPIGYLYANECRPGYSGRPF-----STICLN-- 81  
+P LP PT DF F G+ + Y C PG GR SI C N  
Sbjct: 614 IPGGLP---PTIANGDFISTNRENFHYGSAVYTRCNGSGRKYVELVGPSPVICTSDD 670

Query: 82 --SWTSADKCRKSCRNPPDPVNGMAHVIKD---IQFGSQIKYSCPFGYRLIGSSSA 135  
+W+ +C + PP+ NG+ ++ D +++ C G+ + G  
Sbjct: 671 QVGWMSGAPQCIIPNKCCTPPVANGI--LVSDNRSLFLANVEVFRGQGFVNGPRPV 728

Query: 136 TCIIISGNTVIMDNKTTPVC 153  
C W+ + P C  
Sbjct: 729 KCOALNR--WPELPSC 743

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFPAPFNLTDDP-----EPPIGYLYANECRPGYSGRPF-----STICLN-- 81  
+P LP PT DF F G+ + Y C PG GR SI C N  
Sbjct: 164 IPGGLP---PTIANGDFISTNRENFHYGSAVYTRCNGSGRKYVELVGPSPVICTSDD 220

Query: 82 --SWTSADKCRKSCRNPPDPVNGMAHVIKD---IQFGSQIKYSCPFGYRLIGSSSA 135  
+W+ +C + PP+ NG+ ++ D +++ C G+ + G  
Sbjct: 221 QVGWMSGAPQCIIPNKCCTPPVANGI--LVSDNRSLFLANVEVFRGQGFVNGPRPV 278

Query: 136 TCIIISGNTVIMDNKTTPVC 153  
C W+ + P C  
Sbjct: 279 KCOALNR--WPELPSC 293

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPPIGLYANECRPGYS-GRPSII-----CLK-----NSWTSADKCRK--SCRNPP 99  
+ P G ++Y C G P++I C N W+S ++C +P  
Sbjct: 1792 DIPYGRKISYACDHPDRGTRTNLIGESIRCTSDPQNGWSPAPRCLESLVPAACPPP 1851

Query: 100 EPPVNGM--AHVITDIQFGSQIKYSCPFGYRLIGSSSANCIIISGNTVIMDNKTTPVC 153  
P NG HV + G I Y+C GY L+G C G IW C

Sbjct: 1852 EKIQNGHYIGWHSVLYLP-GMTISTYTCDDPYLLVGKGFIFCTDQ---IWSOLDHYC 1904

Score = 36.7 bits (83), Expect = 0.12  
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PTNLTDDP-----EPPIGYLYANECRPGYSGRPF-----STICLN--SWTSADK 88  
PT DF P GT + Y+C G G SI C W+S  
Sbjct: 1523 PTISNDPYSNKRTHNGTAVTVOCHGDPGQQLVELGERSITCTSDQVWSSSP 1582

Query: 89 DKCKRSCRNPPDPVNGMAHVIKDIOFGSQ---IKYSCRGYRLIGSSSANCIIISGNTVY 145  
+C + P+ N + V + P S I++ C G+ ++G+ C +G  
Sbjct: 1583 PRCTINCTAPFEVEMAI-RVPGNRSPFSLTEIIRRCQPGFVWVGSHTVOCQNGR--- 1638

Query: 146 WDNKTTPVC 153  
W K P C  
Sbjct: 1639 WGEKLPNC 1646

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFPAPFNLTDDPPEPIGYLYANECRPGYS-GRPSII-----CLK---NSV 83  
C P +P R P + PP G +NY C P G P +I C N V  
Sbjct: 421 CPSPFVIRNGRHGKPLEV-PPFGKAVNYTCDPHDRGTSFDLIGESTRICTSDPQNGV 479

Query: 84 WTSADKCRK-RKSCRNPPDPVNGMAHVIKDIOFGSQIKYSCPFGYRLIGSSSANCII 139  
W+S +C C+ P + D G+ +KY C Y S NC+  
Sbjct: 480 WSPAPRCGILGHCOAHPDLFPAKLTQTNASDPPIGTSIAKTECHPEY-YGRPSITCL- 537

Query: 140 SGNTVIMDNKTTPVC 153  
++W+ + VC  
Sbjct: 538 --DNLWSSPDDVC 549

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFPAPFNLTDDPPEPIGYLYANECRPGYS-GRPSII-----CLK---NSV 83  
C P +P R P + PP G +NY C P G P +I C N V  
Sbjct: 871 CPSPFVIRNGRHGKPLEV-PPFGKAVNYTCDPHDRGTSFDLIGESTRICTSDPQNGV 929

Query: 84 WTSADKCRK-RKSCRNPPDPVNGMAHVIKDIOFGSQIKYSCPFGYRLIGSSSANCII 139  
W+S +C C+ P + D G+ +KY C Y S TC+  
Sbjct: 930 WSPAPRCGILGHCOAHPDLFPAKLTQTNASDPPIGTSIAKTECHPEY-YGRPSITCL- 987

Query: 140 SGNTVIMDNKTTPVC 153  
++W+ + VC  
Sbjct: 988 --DNLWSSPDDVC 999

>GSEBQ:AAK41010 Human polypeptide SEQ ID NO 5941.  
Length = 2044

Score = 256 bits (647), Expect = 8e-68  
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLIALALVLLISFS-DCNVPEMLPFPAPFNLTDDPPEPIGYLYANECRPGYSGRPSII 76  
G LLA +VLL + QCN PEMLPFPAPFNLTDDPPEPIGYLYANECRPGYSGRPSII  
Sbjct: 30 GSLLAVVLLALVAMGQCNAPFEMLPFPAPFNLTDDPPEPIGYLYANECRPGYSGRPSII 89

Query: 77 ICLKNSVWTSADKCRKSCRNPPDPVNGMAHVIKDIOFGSQIKYSCPFGYRLIGSSSANCII 136  
ICLKNSVWTSADKCRKSCRNPPDPVNGMAHVIKDIOFGSQIKYSCPFGYRLIGSSSANCII  
Sbjct: 90 ICLKNSVWTSADKCRKSCRNPPDPVNGMAHVIKDIOFGSQIKYSCPFGYRLIGSSSANCII 149

## BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

Query: 137 CIISGNTVIMDNKTPVCD 154  
CIISG+TVIMDN+TP+CD  
Sbjct: 150 CIISGDTVIMDNETPICD 167

Score = 176 bits (442), Expect = 9e-44  
Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSFDQCNVPEMLPEARPTNLTDDEFPBIGTVLNTCECRPGVSGRPFSSICLKNSVWISA 87  
LS + C PE PPA PT +DEFP+GT LNTCECRPGV G+ FSI CL+N VM+S  
Sbjct: 1394 LSVRAGHGCKTPEQFPASPPIPIINDFEFVVGTSLNTECRPGVGTGRKFSISCLENLWSSV 1453

Query: 88 KQCKRKSCRNPPDPVNGMAHVIKDIOFQSQIKYSCPEKGYRLIGSSATCIISGNTVIMD 147  
+D C+RKSC PP+P NGM H+ D QFGS + YSC +G+RLIGS S TC++SGN V MD  
Sbjct: 1454 EDNCRKRS CGPPEPENGMIHINDYQFSTVANS CNEGFRLLGSSPTVCLVSGNNVTMD 1513

Query: 148 NKTPVCD 154  
K P+C+  
Sbjct: 1514 KKAIPICE 1520

Score = 166 bits (417), Expect = 8e-41  
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 CNVEMLEPAPPTNLTDPEPPIGTLYNVECRPEXSGRPFSTICLNKSNVWTSAAKRCRK 94  
C P+ PA+ T+ +EPIGT L YECP Y GRPST CL N VM+S KD CKRK  
Sbjct: 948 CQAPDHPLPAKLQTQNASDPFGISLTKYCRPEYGNRPFSTICLDNLVWSSPKDVCCKRK 1007

Query: 95 SCRNPDPVNGMAHVINDIQSGSLKYSCEKGYNLIGSSANCIISGNTVITWDNKT7VC 153  
SC+ PPDVNGM HVI DIQ GS+I YSC G+ALIG SSA CI+SGNT W K P+C  
Sbjct: 1008 SCRPPDPVNGMAHVINDIQGSRINYSCTTGHLNIGHSAECLISGNTVAHNSKTPDIC 1066

Score = 164 bits (412), Expect = 3e-40  
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVEEWLFAPRPNVLTDDEFPICGYLVNVECRPGVSGRPISITCLKNSVMTSAKDCKRK 94  
C P+ FA+ T+ +FPIGT L YECRP Y GRPSI CL N VM+S KD CKRK  
Sbjct: 498 COADPHFLPAKLKQTMASDPFPGTSLKYECRPETVYGRPSITCLDNLVWSSPKDVCRRK 557

Query: 95 SCRNPDPVNGMAHYIKDIQFGSGQIKRSCPKRYRLIGSSATCIIISGNTVIMDKTTPVC 153  
SC+ PDPDPVNGM HVI DIQ GS+I YSC G+RLIG SCA C+SGN W K P+C  
Sbjct: 558 SCKTDPDPVNGMAYITTDIQVGSRIINSCCTGHRLLIGHSAECILSGNAAHMSZKPPIC 616

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSFSDQCNVEMWLPFARPTNLWDPFEPDGYLTANECRPSYSGR - PPSIICLNKSNVWTS 86  
L S S C P + A ↑ D P G + Y C P G Y R S + C W +  
Subject: 745 LPSGSRVCCPDPVDVLIHAETQRKD-NFSPGQEVFSCPEFYDLGGAASNRCTPQGMSP 803

```

Query: 87 AKDKCKRKSCRN-PPDPVNGMAHYIKDIQFGSGLKYSCKPKYRLIGSSATCIIGNTVI 145
      A C+KSC + +NG + +Q G+++ + C +G+L GSS++ C+++ +
Sbjct: 804 AAPTEVKSQDDFMQOLNGRVLPFVNIQLGAKVDVFCDBEFGOLGSSASVYCVLAGMSL 863

```

```
Query: 146 WDNKTPVCD 154
      W++ PVC+
sbjct: 864 WNSSVPVCE 877
```

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFDQCNVPEMLPFAFPTNLDDFEPPIGYLVNVECRPGYSGR-PFSIICLKNSVWTS 86

15 of 56

5/5/03 8:58 PM

16 of 56

5/5/03 8:58 PM

L S S C P + A T D F G + Y C P G Y R S + C W +  
 Sbjct: 295 LSCSRVCGPPVLAHAFQDKD-NFSPGQEVYSCSPEDYDLGAASNRCPQGDWSP 353  
 Query: 87 ADCKKRSGRN-PPDPVNGMAHVTKDQIGSKISYCSKRGTHLIGSSANCIISGNVI 145  
 A C + KSC + NG +AQ GAAA + C +G+L L GSS+ C+ +G  
 Sbjct: 354 AATPCVCSMDPMDGOLLINRSLVFPVNLQGLKSLVPSLSSASVACVATGSL 413

Query: 146 WDNKTPVCD 154  
W++ PVC+  
Sbjct: 414 WNSSVPVCE 422

Score = 64.8 bits (155), Expect = 4e-10  
Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)

Query: 28 LSSPFDQCNVPEWLPFAFPTNLTDDEPPEIGTYLNYECRPGISGR-PFSIICLKSNWTS 86  
L S S C P + T D P G + Y C PGY R S + C W +  
Sbjct: 1195 LPSCRCVQPPPELIGHTPSHD-NRSPGQETVYSCBPYDLRGAASLHCTPQGDWSP 12

```

Query: 87 AKDKCKRKSCKRNPPDV-NQMAHWIKDIOFGSQIKYSCCKGYRLIGSSATCIISGNVI 145
      +C KSC + +G ++Q G+++ + C +G+RL GSS + C++ G +
Sbjct: 1254 EAPRCVAKSCDDFLGQLPHCRVLPFLNLQLGAKVSFVCEGFRLLKGSVSVSHCVLVGMRSL 1313

```

```
Query: 146 WDNKTPVCD 154
      W+N PVC+
Sbjct: 1314 WNNNSVPVCE 1322
```

Score = 61.3 bits (146), Expect = 5e-09  
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 LTDDPEFPIGYLANTECRPGYSGR-PFSITCLKUSVWTSKAKDKCKRKSCHRNPPDPV-NGM 106  
 L+ F G + Y C P Y R S+ C W+ +C KSC + +G  
 Subject: 1668 LSHQNPSPGQVFSCEPSTDLRGAISLHCTPGQDWSPEAFRCVWKSODDFLGQLPHGR 1727

Query: 107 AHVAKDIOFGSQIKYSCPGYRLIGSSATCIISGNTVIMDKTPVCD 154  
+ ++Q G+++ + C +G+RL G S++ C+++G ++W+ PVC+  
Sbjct: 1728 VLLPLNLQLGAKVSPVCDGFRILKGRASHCVLAGKALMNSSVPCE 1775

Score = 48.0 bits (112), Expect = 5e-05  
Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)

Query: 26 LLSGSPDOCNV----PEMLPAPRPNLNDPEEPICGYIYINCRPGYS--GRPEIICL 79  
L+ SS D C P PF ++ D +P G+ +NY C G+ G P S CL  
Subject: 1448 LVMSSEVDNCRKSCGPPPEPNNGMHINDYQ--GSVYVSCNEGRRLTGP-STYCL 150

```

Query: 80  ---KNSVWTSADKCKRKSCHNPPDPVNGMAHVIDIQF--GSQIKYSCPKG-----YR 128
          N  W      C+  SC  PP  NG  +      F  G+ +  Y  C  G      +
Sbjct: 1505 VSGNNVTWDKAPICELISCCEPPTISNGDFYSNNRNTSPFHNGTVVYYQCHTGDPDEQLFE 1566

```

Query: 129 LIGSSATCIISGNTV-IWDNKTPTVCDSLK 158  
L+G S C + V +W + P C S K  
Sbjct: 1565 LVGEISIVCTSKDDQVGWSSPPRCISLTK 1599

Score = 43.8 bits (101), Expect = 9e-04  
Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)

```

Query: 58  GYLVNVEGRPGYS--GRPFSICLKNSVWTSAKDKCKRRKSCRNPPDPVNGMAHVI--KD 112
           G  +YY C PGY  G+ F I C      +W+      CK  +C  P  +NG++  +  K
Sbjct: 1875 GMTISYVCDPGVLVNGKF-IPCTDGIWSQLDHYCKEKNCSFPLE-MNGISKLEMKRV 193

```

Query: 113 IQFGSQRKYSCKPKGYRLIGSSSACITISGNTVIMDNKTPVCDSEIKYAFL 162  
+G + C GY L GS + C WD C S A +

Sbjct: 1933 YHGDVYTLKCEDGYTLGSSPMSCOADR--WDEPLACTSRTHDALI 1979

Score = 43.8 bits (101), Expect = 9e-04

Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTYLANECPGV---SGRPSIICLNKNSVTSKDKCRKSCNPPDPVNG--MAHVI 111

Sbjct: 129 GSQIKYSCGKYLIGSSATCIIISDVTWNETPICRILPCGLPTITMDGISTNE 188

Query: 112 DIFGSOIKYSCPKG-----YRLIGSSATCIIISGNTV--IMDKRTPVC 153

Sbjct: 189 NFHGSVVTYRCNPGSGGRKVFELVGEPSICTSNDQVIGMSPAQC 237

Score = 43.0 bits (99), Expect = 0.002

Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGYLANECPGV---GRPSIICLNKNSV--WTSADKCRKSCNPPDPVNG--MA 107

Sbjct: 575 DIFGSRINYSCTTGRLIGHSSAECIIISGNAHMSRPPICRILPCGLPTITMDGISTNE 634

Query: 108 HVIKDIFGSOIKYSCPKG-----YRLIGSSATCIIISGNTV--IMDKRTPVC 153

Sbjct: 635 TNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSICTSNDQVIGMSPAQC 687

Score = 43.0 bits (99), Expect = 0.002

Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGYLANECPGV---SGRPSIICLNKNSVTSKDKCRKSCNPPDPVNG--MAHVI 110

Sbjct: 1283 LKAKYSPVCDGGRKLGSSVSHCVLWGRSLMNSVPCHEICRPFALLNGHTRPS 1342

Query: 111 KDIFGSOIKYSCPKG-----KGRILIGSSATCIIIS--GNTVIMDKRTPVCSEIA 158

Sbjct: 1343 GDIPGRKISYTCDDPHDRGNTFNLIGESTIRCTSDPHGNGV--WSPAPRCLESTV 1397

Score = 42.6 bits (98), Expect = 0.002

Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGYLANECPGVSGRPPS---IICLNKNSVTSKDKCRKSCNPPDPVNG--MA 107

Sbjct: 1025 DIFGSRINYSCTTGRLIGHSSAECIIISGNTVIMDKRTPVCICRILPCGLPTITMDGISTNE 1084

Query: 108 HVIKDIFGSOIKYSCPKG-----YRLIGSSATCIIISGNTV--IMDKRTPVC 153

Sbjct: 1085 TNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSICTSNDQVIGMSPAQC 1137

Score = 42.6 bits (98), Expect = 0.002

Identities = 31/112 (27%), Positives = 53/112 (46%), Gaps = 15/112 (13%)

Query: 57 IGYLANECPGV---SGRPPS---IICLNKNSVTSKDKCRKSCNPPDPVNG--MAHVI 110

Sbjct: 1736 LKAKYSPVCDGGRKLGSSVSHCVLWGRSLMNSVPCHEICRPFALLNGHTRPL 1795

Query: 111 KDIFGSOIKYSCPKG-----KGRILIGSSATCIIIS--GNTVIMDKRTPVCSEIA 154

Sbjct: 1796 GDIPGRKISYTCDDPHDRGNTFNLIGESTIRCTSDPHGNGV--WSPAPRCLESTV 1846

Score = 41.4 bits (95), Expect = 0.005

Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGYLANECPGV---SGRPSIICLNKNSVTSKDKCRKSCNPPDPVNGMAHVIKD 112

Sbjct: 383 LKAKYSPVCDGGRKLGSSVSHCVLWGRSLMNSVPCHEICRPFALLNGHTRPS 441

Query: 113 IQ---FSGQIKYSCPKG-----KGRILIGSSATCIIIS--GNTVIMDKRTPVC 153

Sbjct: 442 LEVFPGRKAVNTYCDPHDRGNTFNLIGESTIRCTSDPHGNGV--WSPAPRCLESTV 492

Score = 41.4 bits (95), Expect = 0.005

Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGYLANECPGV---SGRPSIICLNKNSVTSKDKCRKSCNPPDPVNGMAHVIKD 112

Sbjct: 833 LKAKYSPVCDGGRKLGSSVSHCVLWGRSLMNSVPCHEICRPFALLNGHTRPS 891

Query: 113 IQ---FSGQIKYSCPKG-----KGRILIGSSATCIIIS--GNTVIMDKRTPVC 153

Sbjct: 892 LEVFPGRKAVNTYCDPHDRGNTFNLIGESTIRCTSDPHGNGV--WSPAPRCLESTV 942

Score = 38.7 bits (88), Expect = 0.030

Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPIGYLANECPGV---GRPSIICLNKNSV--WTSADKCRKSCNPPDPVNG--MA 107

Sbjct: 1797 DIFGSRINYSCTTGRLIGHSSAECIIISGNAHMSRPPICRILPCGLPTITMDGISTNE 1856

Query: 100 PDPVNGM---AHVIKDIFGSOIKYSCPKG-----YRLIGSSATCIIISGNTVIMDKRTPVC 153

Sbjct: 1857 PKIQNHITGHSVLYLP--GNTVIMDKRTPVCSEIA--IMSDIHC 1909

Score = 37.5 bits (85), Expect = 0.067

Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEWLPAPRPTNLTDLP-----EPIGYLANECPGVSGRPPS---IICLNKNSV 81

Sbjct: 619 IPCGLP---PTIANGDPISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSICTSND 675

Query: 82 --SWTSADKCRKSCNPPDPVNGMAHVIKD---IQGSOIYSCPKGRLIGSSA 135

Sbjct: 676 QVIGMSGAPQCIIPNKCPTPVNENG--LVEDNNSLFLSLNVEFPCQGFVMEGPRPV 733

Query: 136 NCIIISGNTVIMDKRTPVC 153

Sbjct: 734 KQALNR---WEPELPSC 748

Score = 37.5 bits (85), Expect = 0.067

Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEWLPAPRPTNLTDLP-----EPIGYLANECPGVSGRPPS---IICLNKNSV 81

Sbjct: 169 IPCGLP---PTIANGDPISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSICTSND 225

Query: 82 --SWTSADKCRKSCNPPDPVNGMAHVIKD---IQGSOIYSCPKGRLIGSSA 135

Sbjct: 226 QVIGMSGAPQCIIPNKCPTPVNENG--LVEDNNSLFLSLNVEFPCQGFVMEGPRPV 283

Query: 136 NCIIISGNTVIMDKRTPVC 153

Sbjct: 284 KQALNR---WEPELPSC 298

Score = 36.7 bits (83), Expect = 0.12  
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PNTLTDPE-----EPPIGYLVNVECRPGYSGRP-----SIICLKN-----SWTSAX 88  
PT DF F GT + Y+C G G SI C VM+S  
Sbjct: 1528 PTISGDFYSNNRNSFHNHGVTVYQCHNGDGEQLFELVGENSIYCTSKDQVGVWSSSP 1587  
Query: 89 DKCRKSCNPPDPVNGMAHVIKDIQFSGQIKYSCPKRGYRLIGSSSANTCI 145  
+C + P+ N + V + P S I++C G++G+ C +G  
Sbjct: 1588 PRCISTNKACABEYENAI-RVGNRNSFSFLTEHFRQCGFVNGSHVYQCGVNR--- 1643  
Query: 146 WDKTPVC 153  
W K P C  
Sbjct: 1644 WQKLPHC 1651

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPTNLTDPEPIGYLVNVECRPGYS-GRPFSII-----CLK---NSV 83  
C P +P R T + PP G +NY C P G F +I C N V  
Sbjct: 426 CPEPVIYNRNGHNGKPLEV-FPPGKAVNYTCDPHDRGTSFLIGSTRCTSDPQNGV 484  
Query: 84 WTSADKCK-RKSCNPPDPVNGMAHVIKDIQFSGQIKYSCPKRGYRLIGSSSANTCI 139  
W+S +C C+ P + D C+ +RY C Y S TC+  
Sbjct: 485 WSSPAPRCGLGHCAFDHFLPAKLKQYMASDPPIGTSIKYECRPEY-YGRPFSITCL- 542  
Query: 140 SGNVTYIMDKTPVC 153  
+ +W + VC  
Sbjct: 543 --DNLWSSPRDVC 554

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPTNLTDPEPIGYLVNVECRPGYS-GRPFSII-----CLK---NSV 83  
C P +P R T + PP G +NY C P G F +I C N V  
Sbjct: 876 CPEPVIYNGHNGKPLEV-FPPGKAVNYTCDPHDRGTSFLIGSTRCTSDPQNGV 934  
Query: 84 WTSADKCK-RKSCNPPDPVNGMAHVIKDIQFSGQIKYSCPKRGYRLIGSSSANTCI 139  
W+S +C C+ P + D C+ +RY C Y S TC+  
Sbjct: 935 WSSPAPRCGLGHCAFDHFLPAKLKQYMASDPPIGTSIKYECRPEY-YGRPFSITCL- 992  
Query: 140 SGNVTYIMDKTPVC 153  
+ +W + VC  
Sbjct: 993 --DNLWSSPRDVC 1004

>GSEQ:AM39224 Human polypeptide SEQ ID NO 2369.

Length = 2044

Score = 256 bits (647), Expect = 8e-68  
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLALVALLSSFS-DQCNVPEMLPFARPTNLTDPEPIGYLVNVECRPGYSGRPSI 76  
G LLA AYLL + QCN PMLPFARPTNLTDPEPIGYLVNVECRPGYSGRPSI  
Sbjct: 30 GSLLAVVLLALVAMGQNAEMLPFARPTNLTDPEPIGYLVNVECRPGYSGRPSI 89  
Query: 77 ICLNSWTSADKCKRKSCNPPDPVNGMAHVIKDIQFSGQIKYSCPKRGYRLIGSSSANT 136  
ICLNSWTSADKCKRKSCNPPDPVNGMAHVIKDIQFSGQIKYSCPKRGYRLIGSSSANT  
Sbjct: 90 ICLNSWTSADKCKRKSCNPPDPVNGMAHVIKDIQFSGQIKYSCPKRGYRLIGSSSANT 149  
Query: 137 CIISGNTVIMDKTPVC 154  
CIISG+TVIMDN+TP+CD

Sbjct: 150 CIISGNTVIMDKTPVC 167

Score = 176 bits (442), Expect = 9e-44  
Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSPDOCNVPEMLPFARPTNLTDPEPIGYLVNVECRPGYSGRPSIICLKNWTSAXDKCKR 87  
LS + C PE PFA PT +DEFP+QT IYECRPGY G+ PSI CL+N VM+S  
Sbjct: 1394 LSVRAGCKTPQGPFPASPPIPIINDFEPIYSLNVECRPGYRGMGFISCLKNWTSAX 1453  
Query: 88 KRCRKSCNPPDPVNGMAHVIKDIQFSGQIKYSCPKRGYRLIGSSSANTCIISGNTVIM 147  
+D C+KSCC PP+P NCM H+ D QFOS + YSC +GRLLG S TC++SGN V MD  
Sbjct: 1454 EDNCRKSCGPFEPFNGVHNTDQFSTVYSCNGBRLLIGSSTYCLVSGNVTMD 1513  
Query: 148 NRTVPCD 154  
K P+C+  
Sbjct: 1514 KRAPICE 1520

Score = 166 bits (417), Expect = 8e-41  
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 CNVPEMLPFARPTNLTDPEPIGYLVNVECRPGYSGRPSIICLKNWTSAXDKCKR 94  
C P+ FA+ T+ +PPIGT L YECRP Y GRPFSI CL N VM+S KD CKR  
Sbjct: 948 CQAPDHFLPAKLKQYMASDPPIGTSIKYECRPEYGRPFSITCLDNLWSSPRDVCCKR 1007  
Query: 95 SCNPPDPVNGMAHVIKDIQFSGQIKYSCPKRGYRLIGSSSANTCIISGNTVIMDKTPVC 153  
SC+ PDPVNGM HVI DIO GS+I YSC +GRLLG SSA CI+SGNT W K P+C  
Sbjct: 1008 SCRTPEPVGMAHVIKDIQVSRINYSCTGRLIGHSSABRCLISGNTAWSTKPTPIC 1066

Score = 164 bits (412), Expect = 3e-40  
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVPEMLPFARPTNLTDPEPIGYLVNVECRPGYSGRPSIICLKNWTSAXDKCKR 94  
C P+ FA+ T+ +PPIGT L YECRP Y GRPFSI CL N VM+S KD CKR  
Sbjct: 498 CQAPDHFLPAKLKQYMASDPPIGTSIKYECRPEYGRPFSITCLDNLWSSPRDVCCKR 557  
Query: 95 SCNPPDPVNGMAHVIKDIQFSGQIKYSCPKRGYRLIGSSSANTCIISGNTVIMDKTPVC 153  
SC+ PDPVNGM HVI DIO GS+I YSC +GRLLG SSA CI+SGNT W K P+C  
Sbjct: 558 SCRTPEPVGMAHVIKDIQVSRINYSCTGRLIGHSSABRCLISGNTAWSTKPTPIC 616

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSPDOCNVPEMLPFARPTNLTDPEPIGYLVNVECRPGYSGR-PSIICLKNWTSAX 86  
L S S C P + A T D F G + Y C PGY R S+ C W+  
Sbjct: 745 LPSCNVCQPPDVLHAERTQDKD-NFSPQGEVYFSCPEPYDLRGAASNRCTPQGMSP 803  
Query: 87 AKDKCRKSCN-PPDPVNGMAHVIKDIQFSGQIKYSCPKRGYRLIGSSSANTCIISGNTV 145  
A C+ KSC +NG ++Q G+++ + C +G++L GSS++ C++G +  
Sbjct: 804 AALTCBVSQCDPMQLNGRVLPVNIQLAKAVDVDEDFQKLKSSASVCYLAEMSL 863  
Query: 146 WDKTPVC 154  
W++ PNC+  
Sbjct: 864 WNSVYCE 872

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSPDOCNVPEMLPFARPTNLTDPEPIGYLVNVECRPGYSGR-PSIICLKNWTSAX 86  
L S S C P + A T D F G + Y C PGY R S+ C W+  
Sbjct: 295 LPSCNVCQPPDVLHAERTQDKD-NFSPQGEVYFSCPEPYDLRGAASNRCTPQGMSP 353

Query: 87 AKDKCKRCKSN--PPDPVNGAHVINDIOFSGQIKYSCPKGRLIGSSSACIIISGNTV 145  
A C+ KSC + +NG + +Q C++ + C +G+L GSS++ C++G +  
Sbjct: 354 AATPCVATSCDDPFGQLANGVLEPVNDQAKVDFVCDGRLGSSSAYCVLAGESL 413

Query: 146 WDKRTPVCD 154  
W++ PVC+  
Sbjct: 414 WNSSVPCVCE 422

Score = 64.8 bits (155), Expect = 4e-10  
Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)

Query: 28 LSSFDQCNVEMLPAPRNLTDDPEPIGTILATECRPGYSR--PFSIICLNKSNVWTS 86  
L S S C P + + D F G + Y C PGY R S+ C W+  
Sbjct: 1195 LPSCSRVCOPPEILAGEHPHSHOD--NFPQOEYVSCPEYDLRGAASLHCTPOQWSP 1233

Query: 87 AKDKCKRCKSNPPDPV--NGAHVINDIOFSGQIKYSCPKGRLIGSSSACIIISGNTV 145  
+C KSC + +G + +Q C++ + C +G+L GSS + C++ G +  
Sbjct: 1254 EAPRCAYKSCDDPLGLPHGRVLPPLNQLAKVSVCDGFRILKGSVSHCVLWGRSL 1313

Query: 146 WDKRTPVCD 154  
W+N PVC+  
Sbjct: 1314 WNSVPCVCE 1322

Score = 61.3 bits (146), Expect = 5e-09  
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 LTDDPEPIGTILATECRPGYSR--PFSIICLNKSNVWTSADCKRCKSNPPDPV--NG 106  
L+ F G + Y C P Y R S+ C W+ +C KSC + +G  
Sbjct: 1668 LSHQDNFSPQOEYVSCPEYDLRGAASLHCTPOQWSPBAPRYKSCDDPLGLPHGR 1727

Query: 107 AHVINDIOFSGQIKYSCPKGRLIGSSSACIIISGNTVINDKRTVPCD 154  
+ + +Q G++ + C +G+L G S+ +C++G +W++ PVC+  
Sbjct: 1128 VLLPLNQLAKVSVCDGFRILKGSASHCVLAKALMNSVPCVCE 1775

Score = 48.0 bits (112), Expect = 5e-05  
Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)

Query: 26 LLLSFDQCNV---PEMLPAPRNLTDDPEPIGTILATECRPGYS--GRPFSIICL 79  
L+ SS D C P PF ++ D +F G+ +NY C G+ G P S CL  
Sbjct: 1448 LWMSSVEDNCRKSKGPPPEPFGMHIINDYQF--GSTVWYSCNGRFLIGSP-STYCL 1504

Query: 80 ---KSNVWTSADCKRCKSNPPDPVNGAHVINDIOF--GSOIKYSCERG-----YR 128  
N W C+ SC PP NG + F G+ + Y C G +  
Sbjct: 1505 VSGNNVWMDKAPICELIISCEPPTISNGDPYNNNTSFHNGTVVYQCHGPDGQLPE 1564

Query: 129 LIGSSSACIIISGNTV--INDKRTVPCDSELK 158  
L+G S C + V +W + P C S R  
Sbjct: 1565 LVGRSIVYCTSKDQVGVWSSPPRCISTNK 1595

Score = 46.5 bits (108), Expect = 1e-04  
Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)

Query: 57 IGTILATECRPGY--SGRPFSS--IICLNKSNVWTSADCKRCKSNPPDPVNG--MAHYI 110  
+G + + + C G+ GR S + + +W S+ C++ C NP +NG  
Sbjct: 1736 LQAKVSVCDGFRILKGSASHCVLAKALMNSVPCVDFICFPALINGHRTGTFP 1795

Query: 111 KDIOFSGQIKYSCP-----KGRILIGSSSACII--GNTVINDKRTVPCD 154  
DI +G +I Y+C + LIG SS C GN V W + P C +  
Sbjct: 1796 GPIPYGREISVACDTHPDRCGMPFNILIGSSIRCTSPDQGNV--WSPAPRCE 1846

Score = 43.8 bits (101), Expect = 9e-04  
Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)

Query: 58 GTYILATECRPGYS--GRPFSIICLNKSNVWTSADCKRCKSNPPDPVNGAHV--RD 112  
G + + Y C PGY G+ F I C +W+ CK +C P +NG++ + R  
Sbjct: 1875 GNTISYTCDDPGYLVGKGF--IFCTDQIGMSQLDHCKVNCSPFLF--NMGISRELEKRY 1932

Query: 113 IOFSGQIKYSCPKGRLIGSSSACIIISGNTVINDKRTVPCDSELKVAPL 162  
+G + C GY L GS + C MD C S A +  
Sbjct: 1933 YHGDYVTLAKCEDGYTLESGFMSQCDADR---WDPLAKTSTRADALII 1979

Score = 43.8 bits (101), Expect = 9e-04  
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTYILATECRPGY--SGRPFSS--IICLNKSNVWTSADCKRCKSNPPDPVNG--MAHYI 111  
G+ + Y C GY S II +W + C R C PP NG ++ +  
Sbjct: 129 GSOIKYSCPKGRLIGSSSACIIISGNTVINDNETPICRIPCGLPPTIANGDFISTNRE 188

Query: 112 KDIOFSGQIKYSCP-----YRLIGSSSACIIISGNTV--INDKRTVPC 153  
+ +GS + Y C G + L+G S C + + V IW P C  
Sbjct: 189 NPHYSVVTTRCNPSGGRKVFELVBSPTICTSNDQVGIWSPAPQC 237

Score = 43.0 bits (99), Expect = 0.002  
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTILATECRPGYS--GRPFSIICLNKSNV--WTSADCKRCKSNPPDPVNG--MA 107  
+ +G+ +NY C G+ G + L + W++ C+R C PP NG ++  
Sbjct: 575 DIVQSRINSCCTGHRILHGSABECLISGNAAWSTKRPICQILPGCLPTIANGDFIS 634

Query: 108 HVIKDIOFSGQIKYSCP-----YRLIGSSSACIIISGNTV--INDKRTVPC 153  
+ + +GS + Y C G + L+G S C + + V IW P C  
Sbjct: 635 TNRNHFHGSVVTTRCNPSGGRKVFELVBSPTICTSNDQVGIWSPAPQC 687

Score = 43.0 bits (99), Expect = 0.002  
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGTILATECRPGY--SGRPFSS--IICLNKSNVWTSADCKRCKSNPPDPVNG--MAHYI 110  
+G + + + C G+ S ++ S+W ++ C+ C NP +NG  
Sbjct: 1283 LQAKVSVCDGFRILKGSVSHCVLWGRBLMNSVPCVCHIRCPAPRALINGHRTGTS 1342

Query: 111 KDIOFSGQIKYSCP-----KGRILIGSSSACIIIS--GNTVINDKRTVPCDSELK 158  
DI +G +I Y+C + LIG S+ C GN V W + P C + +  
Sbjct: 1343 GPIPYGREISVACDTHPDRCGMPFNILIGESTIRCTSDPHGNV--WSPAPRCELSVR 1397

Score = 42.6 bits (98), Expect = 0.002  
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTILATECRPGYSRPFSS--IICLNKSNVWTSADCKRCKSNPPDPVNG--MA 107  
+ +G+ +NY C G+ S ++ S+W ++ C+ C NP +NG  
Sbjct: 1025 DIVQSRINSCCTGHRILHGSABECLISGNAAWSTKRPICQILPGCLPTIANGDFIS 1084

Query: 108 HVIKDIOFSGQIKYSCP-----YRLIGSSSACIIISGNTV--INDKRTVPC 153  
++ +GS + Y C G + L+G S C + + V IW P C  
Sbjct: 1085 TNRNHFHGSVVTTRCNLIGSRKVFELVBSPTICTSNDQVGIWSPAPQC 1137

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTILATECRPGY--SGRPFSS--IICLNKSNVWTSADCKRCKSNPPDPVNGAHVIND 112

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTALNTECRPGY-----SGRPFSLICLNKSVTSADKCKRSCRNPDVNGMAHYKD 112  
+G +++ C G+ S ++ S+W S+ C++ C +P NG H K  
+P LP PT DF P G+ + Y C PG GR SI C N  
Sbjct: 813 LGAKVDFVCEQGLKSSASVCYLKAGMSLMSNVCEIFCPSPVTPWG-RHTGKP 891

Query: 113 IQ---FSGQIKYSCP-----KGYRLIGSSANCTII--SGNTVIMDKKTPVC 153  
++ FG + Y+C + LIG S+ C GN V W + P C  
Sbjct: 442 LEVFPFGKAVNYTCDDPHDGTSPDLIGESTIRCTSDPQNGV-WSSPAPRC 942

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFAFPNTLTDPE-----EPPIGTALNTECRPGYSGRPF-----SIICLNK-- 81  
+P LP PT DF P G+ + Y C PG GR SI C N  
Sbjct: 619 IFCGLP---PTINGDFISTNRENFHYSGVYTRCNMGSGKRFELVGEPSITCTSDND 675

Query: 82 --SVTSAKDKCKRCKRSCRNPDVNGMAHYKD---IQFSGQIKYSCPKGYRLIGSSSA 135  
+W+ +C + PP+ NG+ ++ D +++ C G+ + G  
Sbjct: 676 QVGWISGAPQCIIIPKCTPPNVNGI--LVSDNRSLFLNEVVEPRCQPGVKKGRNV 733

Query: 136 TCIIISGNTVIMDKKTPVC 153  
C W+ + P C  
Sbjct: 734 KCOALNK---WEPELPSFC 748

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFAFPNTLTDPE-----EPPIGTALNTECRPGYSGRPF-----SIICLNK-- 81  
+P LP PT DF P G+ + Y C PG GR SI C N  
Sbjct: 169 IFCGLP---PTINGDFISTNRENFHYSGVYTRCNMGSGKRFELVGEPSITCTSDND 225

Query: 82 --SVTSAKDKCKRCKRSCRNPDVNGMAHYKD---IQFSGQIKYSCPKGYRLIGSSSA 135  
+W+ +C + PP+ NG+ ++ D +++ C G+ + G  
Sbjct: 226 QVGWISGAPQCIIIPKCTPPNVNGI--LVSDNRSLFLNEVVEPRCQPGVKKGRNV 283

Query: 136 TCIIISGNTVIMDKKTPVC 153  
C W+ + P C  
Sbjct: 284 KCOALNK---WEPELPSFC 298

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPPIGTYLWECRPGYS-GRPSII-----CLK-----NSVTSADKCKRCKRSCRNPD 99  
+ P G ++Y C G F+I C N W+S +C+ +C +P  
Sbjct: 1797 DTPGKRIYACDHPDRGNTNLGSESTRCTSDPQNGVMSAPAFCELSPACPCHP 1856

Query: 100 EDPVNGH---AHYKIDIQFSGQIKYSCPKGYRLIGSSANCTIIISGNTVIMDKKTPVC 153  
P NG HV + G I Y+C GY L+G C G W C  
Sbjct: 1857 PRIONGHYIGHVSILYLP-GMTISYTCDDPGYLLVKGKIFCTDQG---IWSOLDHYVC 1909

Score = 36.7 bits (83), Expect = 0.12

Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PTNLTDF-----EPPIGTALNTECRPGYSGRPF-----SIICLNK-----SVTSAK 88  
PT DF F GT + Y+C G G SI C W+S  
Sbjct: 1528 PTISNDPFSNNRSTSPHNGTAVVYCHTQPDQDQFELVGESESTICTSDQVGVMSPP 1587

Query: 89 DKCKRSCRNPDVNGMAHYKIDIQFSGQ---IKYSCPKGYRLIGSSANCTIIISGNTV 145  
+C + P+ N + V + P S I++ C G+ ++G + C +G  
Sbjct: 1588 PRCTISNCTAPAEVYAL-I-RVGNRSTSLTIRFCQGRVWVSGHTVQCTNGR---- 1643

Query: 146 WDKKTPVC 153  
W K P C  
Sbjct: 1644 WGFPLPHC 1651

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFAFPNTLTDPEPIGTALNTECRPGYS-GRPSII-----CLK-----NSV 83  
C P +P R T + PP G +NY C P G F+I C N V  
Sbjct: 426 CSPSPVTPNGRHTGKPLEV-FPPGKAVNYTCDDPHDGTSPDLIGESTIRCTSDPQNGV 484

Query: 84 WTSADKCK-RKSCRNPDVNGMAHY---IKDIOFSGQIKYSCPKGYRLIGSSANCTII 139  
W+S +C C+ P + D G+ +XY C Y S TC+  
Sbjct: 485 WSSPAPRCGILGHCAQDHPFLAKIKQTNA SDPIGTSIKYECREY-YGRPFSITCL- 542

Query: 140 SGNTVIMDKKTPVC 153  
+ ++W + VC  
Sbjct: 543 --DNLVWSSPFDVC 554

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFAFPNTLTDPEPIGTALNTECRPGYS-GRPSII-----CLK-----NSV 83  
C P +P R T + PP G +NY C P G F+I C N V  
Sbjct: 876 CSPSPVTPNGRHTGKPLEV-FPPGKAVNYTCDDPHDGTSPDLIGESTIRCTSDPQNGV 934

Query: 84 WTSADKCK-RKSCRNPDVNGMAHY---IKDIOFSGQIKYSCPKGYRLIGSSANCTII 139  
W+S +C C+ P + D G+ +XY C Y S TC+  
Sbjct: 935 WSSPAPRCGILGHCAQDHPFLAKIKQTNA SDPIGTSIKYECREY-YGRPFSITCL- 992

Query: 140 SGNTVIMDKKTPVC 153  
+ ++W + VC  
Sbjct: 993 --DNLVWSSPFDVC 1004

>GSEQ:ABH11782 Human CRI protein homologue, SBO ID NO:2152.  
Length = 2044

Score = 256 bits (647), Expect = 8e-68  
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLAALVLLLSFS-DQCNVPEMLPFAFPNTLTDPEPIGTALNTECRPGYSGRPSI 76  
G LLA +VLL + QCN PEMLPFAFPNTLTD+PEPIGTALNTECRPGYSGRPSI  
Sbjct: 30 GLLAVVLLALPVAMQCNAPEMLPFAFPNTLTDPEPIGTALNTECRPGYSGRPSI 89

Query: 77 ICLKSVTSADKCKRCKRSCRNPDVNGMAHYKIDIQFSGQIKYSCPKGYRLIGSSAT 136  
ICLKSVTSADKCKRCKRSCRNPDVNGMAHYKIDIQFSGQIKYSCPKGYRLIGSSAT  
Sbjct: 90 ICLKSVTSADKCKRCKRSCRNPDVNGMAHYKIDIQFSGQIKYSCPKGYRLIGSSAT 149

Query: 137 CIIISGNTVIMDKKTPVC 154  
CIIISG+TVIMDN+TP+CD  
Sbjct: 150 CIIISGNTVIMDNTPICD 167



<http://patients.incyte.com/8000/csi-bin/SeeServer/SeeServer>

5/5/2019 8:58 PM

5/5/2019 8:58 PM

Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTTAAVTECRPGY----SGRPSTICLKNVWTSADKCKRSCNPPDPVNG--MAHVR 111  
+G + Y C GY S II +W + C R C PP NG ++ +  
Sbjct: 129 GSOIKYSCWGHLLIGSSANCIISDGYVWMDNETPICRIICPLPTIANDISTNME 188

Query: 112 DIOFSGQIKYSCPKG-----YRLIGSSANCIISGNV--IWDNKTTPVC 153  
++ +G S + Y C G +L+G S C + + V IW P C  
Sbjct: 189 NHRFHSVVTYRCNPGSGRKFELVGEPSIYCTSDNDQVIGSGAPQC 237

Score = 43.0 bits (99), Expect = 0.002  
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPPIGTYLATECRPGY--SGRPSTICLKNV--WTSADKCKRSCNPPDPVNG--MA 107  
+G + +N C G+ G + L + W++ C+R C PP NG ++ +  
Sbjct: 575 DIOVSGRINTSCWGHLLIGSSANCIISGNAMWSTKPPICRIICGPIPLIANDGPTS 634

Query: 108 HVIKDIQFSGQIKYSCPKG-----YRLIGSSANCIISGNV--IWDNKTTPVC 153  
++ +G S + Y C G +L+G S C + + V IW P C  
Sbjct: 635 TNRNHFHYSVVTYRCNPGSGRKFELVGEPSIYCTSDNDQVIGSGAPQC 687

Score = 43.0 bits (99), Expect = 0.002  
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGTIYLANTECRPGY----SGRPSTICLKNVWTSADKCKRSCNPPDPVNG--MAHVR 110  
+G + +N C G+ S ++ S+W ++ C+ C NPP +NG  
Sbjct: 1283 LGANVSVCDDEGFRILKGSVSHCVLWGRSLWNNSVPCHEITFCPPHPLIANGHPTPS 1342

Query: 111 KDIOFSGQIKYSCPKG-----KGYRLIGSSANCIIS--GNTVIMDNKTPVCDESELR 158  
DI +G +I Y+C +LIG S+ C GN V W + P C ++  
Sbjct: 1343 GDIPEGRKISYCTDHPDRGMFNLIGESTIRCTSDPHNGV--WSSPAPRCELSTVR 1397

Score = 42.6 bits (98), Expect = 0.002  
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPPIGTYLATECRPGYSGRPPS---ITCLKNVWTSADKCKRSCNPPDPVNG--MA 107  
+G + +N C G+ S ++ S+W ++ C+R C PP NG ++ +  
Sbjct: 1023 DIOVSGRINTSCWGHLLIGSSANCIISGNAMWSTKPPICRIICGPIPLIANDGPTS 1084

Query: 108 HVIKDIQFSGQIKYSCPKG-----YRLIGSSANCIISGNV--IWDNKTTPVC 153  
++ +G S + Y C G +L+G S C + + V IW P C  
Sbjct: 1085 TNRNHFHYSVVTYRCNPGSGRKFELVGEPSIYCTSDNDQVIGSGAPQC 1137

Score = 42.6 bits (98), Expect = 0.002  
Identities = 31/112 (27%), Positives = 53/112 (46%), Gaps = 15/112 (13%)

Query: 57 IGTIYLANTECRPGY--SGRPPS--ITCLKNVWTSADKCKRSCNPPDPVNG--MAHVR 110  
+G + +N C G+ GR S ++ +W S+ C++ C NPP +NG  
Sbjct: 1736 LGANVSVCDDEGFRILKGSVSHCVLWGRSLWNNSVPCHEITFCPPHPLIANGHPTPS 1795

Query: 111 KDIOFSGQIKYSCPKG-----KGYRLIGSS--ATCIIISGNVIMDNKTPVC 154  
DI +G ++ Y+C +LIG S+ T GN V W + P C ++  
Sbjct: 1796 GDIPEGRKISYCTDHPDRGMFNLIGESTIRCTSDPHNGV--WSSPAPRCEL 1846

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTIYLANTECRPGY--SGRPPSTICLKNVWTSADKCKRSCNPPDPVNGMAHVIKD 112  
+G + +N C G+ S ++ S+W S+ C++ C +PP NG H K  
Sbjct: 383 LGAKVDPVCDDEGFRILKGSVSHCVLWGRSLWNNSVPCHEITFCPPHPLIANGHPTPS 441

Query: 113 IQ---FSGQIKYSCPKG-----KGYRLIGSSANCIIS--GNTVIMDNKTPVC 153  
++ FG + Y+C +LIG S+ C GN V W + P C  
Sbjct: 442 LEVFPFGKAVNVTCDPHDRGTSFDLIGESTIRCTSDPHNGV--WSSPAPRCEL 492

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTIYLANTECRPGY----SGRPSTICLKNVWTSADKCKRSCNPPDPVNGMAHVIKD 112  
+G + +N C G+ S ++ S+W S+ C++ C +PP NG H K  
Sbjct: 833 LGAKVDPVCDDEGFRILKGSVSHCVLWGRSLWNNSVPCHEITFCPPHPLIANGHPTPS 891

Query: 113 IQ---FSGQIKYSCPKG-----KGYRLIGSSANCIIS--GNTVIMDNKTPVC 153  
++ FG + Y+C +LIG S+ C GN V W + P C  
Sbjct: 892 LEVFPFGKAVNVTCDPHDRGTSFDLIGESTIRCTSDPHNGV--WSSPAPRCEL 942

Score = 38.7 bits (88), Expect = 0.030  
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPPIGTYLATECRPGY--SGRPSTICLKNV--WTSADKCKRSCNPPDPVNG--MA 107  
+ P G +Y C P G F++I N W+S +C+ +C +P  
Sbjct: 1797 DIOVSGRINTSCWGHLLIGSSANCIISGNAMWSTKPPICRIICGPIPLIANDGPTS 1856

Query: 100 PDPVNGM---AHVTKDIQFSGQIKYSCPKG-----YRLIGSSANCIISGNVIMDNKTPVC 153  
P NG +H +G + I Y+C GY L+G C G IW C  
Sbjct: 1857 PRIONGHYIGHVSILYLP--GNTIISYCTDHPDRGMFNLIGESTIRCTSDPHNGV--WSSPAPRCEL 1909

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPAPRPVNLTDGF-----EPPIGTYLATECRPGYSGRPPS---ITCLKN-- 81  
+P LP PT DF F G+ + Y C PG GR SI C N  
Sbjct: 619 IPCGLP---PTIANGDFISTNRNHFHYSVVTYRCNPGSGRKFELVGEPSIYCTSDND 675

Query: 82 --SVWTSADKCKRSCNPPDPVNGMAHVIKD---IQFSGQIKYSCPKGKGYRLIGSSA 135  
++ +C + PP+ NG+ ++ D ++ C G+ + G  
Sbjct: 676 QVIGTSGAPQCIIINCKCTPPVENGII--LVSDNLSLPLANEVVERPCQPFVWKGPRRV 733

Query: 136 TCIISGNVIMDNKTPVC 153  
C W+ + P C  
Sbjct: 734 KQALNKK---WEPELPSC 748

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPAPRPVNLTDGF-----EPPIGTYLATECRPGYSGRPPS---ITCLKN-- 81  
+P LP PT DF F G+ + Y C PG GR SI C N  
Sbjct: 169 IPCGLP---PTIANGDFISTNRNHFHYSVVTYRCNPGSGRKFELVGEPSIYCTSDND 225

Query: 82 --SVWTSADKCKRSCNPPDPVNGMAHVIKD---IQFSGQIKYSCPKGKGYRLIGSSA 135  
++ +C + PP+ NG+ ++ D ++ C G+ + G  
Sbjct: 226 QVIGTSGAPQCIIINCKCTPPVENGII--LVSDNLSLPLANEVVERPCQPFVWKGPRRV 283

Query: 136 TCIISGNVIMDNKTPVC 153  
C W+ + P C  
Sbjct: 284 KQALNKK---WEPELPSC 298

Score = 36.7 bits (83), Expect = 0.12  
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PNNLTDDP-----EPPIGYLYNTECRPGYSGRPF-----SIICLANK-----SIWMTSAK 88  
PF DP F GT + Y+C G G SI C N V+S  
Sbjct: 1528 PINSNGPISNNRRTFNHGTAVTYOCHNGPGBQLZELVGRSITSTYSDQVSWSSFP 1567

Query: 89 DECKRSKSNPDVPVNGMAHVTKDIQFGSQ--IKYSCPKGYRLIGSSSANCIIISGNTVY 145  
+C + F+ N + V + F S I++ C G+ ++GS + C +G  
Sbjct: 1588 PCTICTKTAPEYENAI-RVPGNSFSPSLTEIRFCRQPGFVWGSHTVOCQNGR--- 1643

Query: 146 WDKNTPVCD 153  
W R P C  
Sbjct: 1644 WGPFLPHC 1651

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/114 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPNLTDDPEPIGYLYNTECRPGYS-GRPSII-----CLK-----NSV 83  
C P +P R T + FP G +NY C P G P +I C N V  
Sbjct: 426 CPSPVPIENGHTGKPLEY-FPFGKAVNYTCDPHDGTSPDLIGESTICTSDPGNGV 484

Query: 84 WTSADKCK-RKSCNRPDPVNGMAHV---IKDIQFGSQIKYSCPKGYRLIGSSSANCII 139  
W+S +C C+ P + D G+ +XY C Y S TC+  
Sbjct: 485 WSSPAPRCGLGHCOAPDHFLPAKLKTQTNASDPPIGTSLATECRPEY-YGRPSTICL- 542

Query: 140 SGNVTYIMDKTPVC 153  
+ ++W + VC  
Sbjct: 543 --DNLVWSSPFDVC 554

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/114 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPNLTDDPEPIGYLYNTECRPGYS-GRPSII-----CLK-----NSV 83  
C P +P R T + FP G +NY C P G P +I C N V  
Sbjct: 876 CPSPVPIENGHTGKPLEY-FPFGKAVNYTCDPHDGTSPDLIGESTICTSDPGNGV 934

Query: 84 WTSADKCK-RKSCNRPDPVNGMAHV---IKDIQFGSQIKYSCPKGYRLIGSSSANCII 139  
W+S +C C+ P + D G+ +XY C Y S TC+  
Sbjct: 935 WSSPAPRCGLGHCOAPDHFLPAKLKTQTNASDPPIGTSLATECRPEY-YGRPSTICL- 992

Query: 140 SGNVTYIMDKTPVC 153  
+ ++W + VC  
Sbjct: 993 --DNLVWSSPFDVC 1004

>GSEQ:ABG00287 Novel human diagnostic protein #278.

Length = 2039

Score = 256 bits (647), Expect = 8e-68  
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLLAALVLLSFS-DOCNPEMLPFARPNLTDDPEPIGYLYNTECRPGYSGRPSI 76  
G LLA +VLL + OCN PEMLPFARPNLTDDPEPIGYLYNTECRPGYSGRPSI  
Sbjct: 25 GSLLAVVLLALPVAMGQCNAPENLPFARNLTDDPEPIGYLYNTECRPGYSGRPSI 84

Query: 77 ICLKNSVWTSADKCKRSKSNRPDPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSANCII 136  
ICLKNSVWTSADKCKRSKSNRPDPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSANCII 144  
Sbjct: 85 ICLKNSVWTSADKCKRSKSNRPDPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSANCII 144

Query: 137 CIISGNTYIMDKTPVC 154  
CIISGNTYIMDKTPVC 154  
Sbjct: 145 CIISGNTYIMDKTPVC 162

Score = 176 bits (442), Expect = 9e-44

Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSPSDQCNPEMLPFARPNLTDDPEPIGYLYNTECRPGYSGRPSIICLKNSVWTSADKCKR 87  
LS + C FE FFA PT +DFEP+GT LNTERRPOT G FSI CL+N VM+S  
Sbjct: 1389 LSVRAAGCTPFPFASPTIINDPEPVGSLNTERRPOYGRFSGKSFISCTENLWSSV 1448

Query: 88 KDKCKRSKSNRPDPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSANCIIISGNTVY 147  
+D C+RSC PP+P NGM H+ D QFGS + YSC +G+RLGS S TC++SGN V WD  
Sbjct: 1449 EDNCRKSCGPEPEFGAMVHINTDQGSVWSCNEGRLIGSPHYCLVAGNNTVD 1508

Query: 148 NKTPVCD 154  
K P+C+  
Sbjct: 1509 KKAPICE 1515

Score = 166 bits (417), Expect = 8e-41  
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 CNVPEMLPFARPNLTDDPEPIGYLYNTECRPGYSGRPSIICLKNSVWTSADKCKR 94  
C P+ FA+ T+ +FPFGT L YECRP Y GRPFSI CL N VM+S KD CKR  
Sbjct: 943 COADPHFLPAKLKTQTNASDPPIGTSLATECRPEYGRPSTICLNDLVWSSPFDVC 1002

Query: 95 SCNRPDPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSANCIIISGNTVYIMDKTPVC 153  
SC+ PDPVNGM HVI DIQ GS+I YSC G+RLIG SSA CI+SGNT W K P+C  
Sbjct: 1003 SCTPDPVNGMAHVTKDIQVGSRLNYSCTTGRLIGHSSABCLISGNTAHWSTKPPIC 1061

Score = 164 bits (412), Expect = 3e-40  
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVPEMLPFARPNLTDDPEPIGYLYNTECRPGYSGRPSIICLKNSVWTSADKCKR 94  
C P+ FA+ T+ +FPFGT L YECRP Y GRPFSI CL N VM+S KD CKR  
Sbjct: 493 COADPHFLPAKLKTQTNASDPPIGTSLATECRPEYGRPSTICLNDLVWSSPFDVC 552

Query: 95 SCNRPDPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSANCIIISGNTVYIMDKTPVC 153  
SC+ PDPVNGM HVI DIQ GS+I YSC G+RLIG SSA CI+SGNT W K P+C  
Sbjct: 553 SCTPDPVNGMAHVTKDIQVGSRLNYSCTTGRLIGHSSABCLISGNTAHWSTKPPIC 611

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSPSDQCNPEMLPFARPNLTDDPEPIGYLYNTECRPGYSGR-PSIICLKNSVWTS 86  
L S S C P + A T D P G + Y C PGT R S+ C W+  
Sbjct: 740 LPSCSNVQPPEDVLHAKRTYDRD-NFSPQEVFISCEPGIDLGAASNRCTPGDMSF 798

Query: 87 AKDKCKRSKSNRPDPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSANCIIISGNTVY 145  
A C+ RSC + NG +Q G+++ + C +G+L GSS++ C+++G +  
Sbjct: 799 AAPTCEVASCDDPMQGLNGRVLPVNIQLAKVDVCDGFGOLKSSASVCLVAGNESI 858

Query: 146 WDKNTPVCD 154  
W++ PVC+  
Sbjct: 859 WNSVPECE 867

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSPSDQCNPEMLPFARPNLTDDPEPIGYLYNTECRPGYSGR-PSIICLKNSVWTS 86  
L S S C P + A T D P G + Y C PGT R S+ C W+  
Sbjct: 290 LPSCSNVQPPEDVLHAKRTYDRD-NFSPQEVFISCEPGIDLGAASNRCTPGDMSF 348

Query: 87 AKDKCKRSKSNRPDPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSANCIIISGNTVY 145  
A C+ RSC + NG +Q G+++ + C +G+L GSS++ C+++G +  
Sbjct: 349 AAPTCEVASCDDPMQGLNGRVLPVNIQLAKVDVCDGFGOLKSSASVCLVAGNESI 408



++ FG +Y+C +LIG S+ C GN V W + P C  
Sbjct: 437 LEVFPFGKAVNYTCDDPHDRGTSFDLIGSTIRCTSDPQNGV-WSSPAARC 487

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTLYANECRPGY-----SGRPSIICLKNSWTSADKCRKSCNPPDPVNGMAHVIKD 112  
+G +++ C G+ S ++ S+W S+ C++ C +P NG H K  
Sbjct: 828 LGAKVDFVQDEGFLQSSASACVLAQMSLVPCVCEQIFCPSPVILENG-RHTCKP 886

Query: 113 IO--FGSQIKYSCP-----KGYRLIGSSATCII--SGNTVIMDKKTPVC 153  
++ FG +Y+C +LIG S+ C GN V W + P C  
Sbjct: 887 LEVFPFGKAVNYTCDDPHDRGTSFDLIGSTIRCTSDPQNGV-WSSPAARC 937

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFARPTNLTDPF-----EPPIGYLANECRPGYSGRPF-----SIICLN-- 81  
+P LP PT DF F G+ +Y C PG GR SI C N  
Sbjct: 614 IPCGLP--PTIANGDFISTRENHFYGSVYTRCNPGSGRKFVELVGEPSIYCTSDND 670

Query: 82 --SWTSADKCRKSCNPPDPVNGMAHVIKD---IQFSQIKYSCPKGYRLIGSSA 135  
+W+ +C + PP+ NG+ ++ D ++ C G+ + G  
Sbjct: 671 QVGWNGAPACIIIPKCTPPIVENGII--LVSDNRSLFSLNEVVEFRQGVKGRPV 728

Query: 136 TCIIISGNTVIMDKKTPVC 153  
C W+ + P C  
Sbjct: 729 KCOALNK---WEPELPSC 743

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFARPTNLTDPF-----EPPIGYLANECRPGYSGRPF-----SIICLN-- 81  
+P LP PT DF F G+ +Y C PG GR SI C N  
Sbjct: 164 IPCGLP--PTIANGDFISTRENHFYGSVYTRCNPGSGRKFVELVGEPSIYCTSDND 220

Query: 82 --SWTSADKCRKSCNPPDPVNGMAHVIKD---IQFSQIKYSCPKGYRLIGSSA 135  
+W+ +C + PP+ NG+ ++ D ++ C G+ + G  
Sbjct: 221 QVGWNGAPACIIIPKCTPPIVENGII--LVSDNRSLFSLNEVVEFRQGVKGRPV 278

Query: 136 TCIIISGNTVIMDKKTPVC 153  
C W+ + P C  
Sbjct: 279 KCOALNK---WEPELPSC 293

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPPIGYLANECRPGYSGRPF-----SIICLN-- 81  
+P LP PT DF F G+ +Y C PG GR SI C N  
Sbjct: 1792 DIPYKISIVACDTHPRGNTFNLIIGESIRCTSDPQNGVWSSPAFCVPAACPHP 1851

Query: 100 PDPVNGMAHVIKD---IQFSQIKYSCPKGYRLIGSSA 153  
P NG HV + G I Y+C GY L+G C IW C  
Sbjct: 1852 KRIQNGHYIGVNSLILP-GMTISTYCDPGYLVNKGFICTMOG---IWSQIDHYC 1904

Score = 36.7 bits (83), Expect = 0.12  
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PTNLTDPF-----EPPIGYLANECRPGYSGRPF-----SIICLN--SWTSAX 88  
PT DF P GR +Y+C G G SI C WM+S

Sbjct: 1523 PTISNGPTNNRTSPFANGVTVYQCHFGPDGQLFELVGRSTVCTSDQVWSSPP 1582

Query: 89 DKCKKSCNPPDPVNGMAHVIKDIOFGSQ---IKYSCPKGYRLIGSSA 145  
+C + P+ N + V + P S I++ C G+ ++G+ C +G  
Sbjct: 1583 PRICISTKCTAPAEVNAI--RVPGNRSFSLTEIRPQCPGVVGSHTVOCOTNRG--- 1638

Query: 146 WDKKTPVC 153  
W K P C  
Sbjct: 1639 WGPRLPHC 1646

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPTNLTDPEPPIGYLANECRPGYSGRPSII-----CLK-----NSV 83  
C P +P R T + PP G +NY C P G P +I C N V  
Sbjct: 421 CPSPPIVINGRHGKPLEV--PPFGKAVNYTCDDPHDRGTSFDLIGSTIRCTSDPQNGV 479

Query: 84 WTSADKCK--RSCNPPDPVNGMAHVI---IKDIOFGSQIKYSCPKGYRLIGSSA 139  
+S +C C+ P + D G+ +Y C Y S TC+  
Sbjct: 480 WSSPAFRGILGHCOAPDHPLFAKLTYQNASDPPIGTSIAKTECRPEY-YGRPSITCL- 537

Query: 140 SGNTVIMDKKTPVC 153  
+ ++W + VC  
Sbjct: 538 --DNVWSSPDDVC 549

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPTNLTDPEPPIGYLANECRPGYSGRPSII-----CLK-----NSV 83  
C P +P R T + PP G +NY C P G P +I C N V  
Sbjct: 871 CPSPPIVINGRHGKPLEV--PPFGKAVNYTCDDPHDRGTSFDLIGSTIRCTSDPQNGV 929

Query: 84 WTSADKCK--RSCNPPDPVNGMAHVI---IKDIOFGSQIKYSCPKGYRLIGSSA 139  
+S +C C+ P + D G+ +Y C Y S TC+  
Sbjct: 930 WSSPAFRGILGHCOAPDHPLFAKLTYQNASDPPIGTSIAKTECRPEY-YGRPSITCL- 987

Query: 140 SGNTVIMDKKTPVC 153  
+ ++W + VC  
Sbjct: 988 --DNVWSSPDDVC 999

>GSEQ\_AAY55751 Human C3b/C4b receptor (CRL) protein.  
Length = 2039

Score = 256 bits (647), Expect = 8e-68  
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLLAALVLLISFS-DQCNVPEMLPFARPTNLTDPEPPIGYLANECRPGYSGRPSI 76  
G LLA +VLL + OCN PEMLPFARPTNLTD+PEPPIGYLANECRPGYSGRPSI  
Sbjct: 25 GSLVAVVLLALPVLMGQNAPEMLPFARPTNLTDPEPPIGYLANECRPGYSGRPSI 84

Query: 77 ICLKNSVWTAKRCKRSCNPPDPVNGMAHVIKDIOFGSQIKYSCPKGYRLIGSSA 136  
ICLKNSVWT AKR+C-RKSCNPPDPVNGMAHVIKDIOFGSQIKYSC PKGYRLIGSSA  
Sbjct: 85 ICLKNSVWTAKRCKRSCNPPDPVNGMAHVIKDIOFGSQIKYSCPKGYRLIGSSA 144

Query: 137 CIISGNTVIMDKKTPVC 154  
CIISG+TVIMDN+TP+CD  
Sbjct: 145 CIISGNTVIMDKKTPVC 162

Score = 176 bits (442), Expect = 9e-44  
Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSFSQDCNVPEMLPPARPNTLTDPEPIGTLYNTECRPGYSGR-PFSITCLKNWTSADKCRK 87  
LS + C PE PFA PT +DEFP+GN LNYECRPGY G+ PSI CL+N VM+S  
Sbjct: 1389 LSVRAGHCKTEQEPFASPTIPINDPEFTVGTSLNTECRPGYSGRPGFAMFISICLENLMWSSV 1448

Query: 88 KDCRCKRSCRRPDPVNGMAHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTVIMDKTPVCD 147  
+D C+KSC PP+P NCH H+ D OFGS + YSC G+RLIG SSA CI+SGNT W R P+C  
Sbjct: 1449 EDNCRKSCGPEPEFNGVHNTDIOFGSVTNVNSCEGRRLIGSPSTICLVSGNNVIMD 1508

Query: 148 NKTPVCD 154  
K P+C+

Sbjct: 1509 KKAPICE 1515

Score = 166 bits (417), Expect = 8e-41  
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 CNVPEMLPPARPNTLTDPEPIGTLYNTECRPGYSGR-PFSITCLKNWTSADKCRK 94  
C P+ FA+ T+ +FPIGT L YECRP Y GRPFSI CL N VM+S KD CRK  
Sbjct: 943 CQADHFLFAKLTQTNASDPPIGSLKRCRPEYGRPFSTICLMLWSSPDVCKRK 1002

Query: 95 SCRNPDVNGMAHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTVIMDKTPVCD 153  
SC+ PDPVNGM HVI DIQ GS+I YSC G+RLIG SSA CI+SGNT W R P+C  
Sbjct: 1003 SCKTPDPVNGMAHVIKDIOGSRINYSCTGHRLLIGSSAECILSGNTAMSTPEPIC 1061

Score = 164 bits (412), Expect = 3e-40  
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVPEMLPPARPNTLTDPEPIGTLYNTECRPGYSGR-PFSITCLKNWTSADKCRK 94  
C P+ FA+ T+ +FPIGT L YECRP Y GRPFSI CL N VM+S KD CRK  
Sbjct: 493 CQADHFLFAKLTQTNASDPPIGSLKRCRPEYGRPFSTICLMLWSSPDVCKRK 552

Query: 95 SCRNPDVNGMAHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTVIMDKTPVCD 153  
SC+ PDPVNGM HVI DIQ GS+I YSC G+RLIG SSA CI+SGN W K P+C  
Sbjct: 553 SCKTPDPVNGMAHVIKDIOGSRINYSCTGHRLLIGSSAECILSGNMAHMKTRPIC 611

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFSQDCNVPEMLPPARPNTLTDPEPIGTLYNTECRPGYSGR-PFSITCLKNWTSADKCRK 86  
L S S C P + A T D P G + Y C PGY R S+C W+  
Sbjct: 740 LPSCSRVCQPPDPVLAERTORDK-NFSPQEVFVSCPEYDLRGAASMCCTPQGMSP 798

Query: 87 ADCKRKRSCRN-PDPVNGMAHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTV 145  
A C+ KSC + +NG +G+ +C +G+L GSS+ C++G +  
Sbjct: 799 AAPTEVKSQDDPMQGLNGRVLPVNLQAKVDCDEGRQKGSASVCIAGNESL 858

Query: 146 WDKTPVCD 154  
W++ P+C+

Sbjct: 859 WNSVFPCE 867

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFSQDCNVPEMLPPARPNTLTDPEPIGTLYNTECRPGYSGR-PFSITCLKNWTSADKCRK 86  
L S S C P + A T D P G + Y C PGY R S+C W+  
Sbjct: 290 LPSCSRVCQPPDPVLAERTORDK-NFSPQEVFVSCPEYDLRGAASMCCTPQGMSP 348

Query: 87 ADCKRKRSCRN-PDPVNGMAHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTV 145  
A C+ KSC + +NG +G+ +C +G+L GSS+ C++G +  
Sbjct: 349 AAPTEVKSQDDPMQGLNGRVLPVNLQAKVDCDEGRQKGSASVCIAGNESL 408

Query: 146 WDKTPVCD 154

Sbjct: 409 WNSVFPCE 417  
W++ P+C+

Score = 64.8 bits (155), Expect = 4e-10  
Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)

Query: 28 LSSFSQDCNVPEMLPPARPNTLTDPEPIGTLYNTECRPGYSGR-PFSITCLKNWTSADKCRK 86  
L S S C P + A T D P G + Y C PGY R S+C W+  
Sbjct: 1190 LPSCSRVCQPPDPVLAERTORDK-NFSPQEVFVSCPEYDLRGAASMCCTPQGMSP 1248

Query: 87 ADCKRKRSCRNPDV-NGMAHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTV 145  
+C KSC + +G +G+ +C +G+L GSS + C++G +  
Sbjct: 1249 EAPRCVNSCDDPLGQLPHRGVLPVNLQAKVSVDCDEGRKGSVSHCVLQGRSL 1308

Query: 146 WDKTPVCD 154  
W+N P+C+

Sbjct: 1309 WNSVFPCE 1317

Score = 61.3 bits (146), Expect = 5e-09  
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 LTDPEPIGTLYNTECRPGYSGR-PFSITCLKNWTSADKCRKSCRNPDV-NGM 106  
L+ F G + Y C P Y R S+C W+ +C KSC + +G  
Sbjct: 1663 LSHQDFSPQEVFVSCPEYDLRGAASLHCTPQGMSPDAPRCVNSCDDPLGQLPHRG 1722

Query: 107 AHVIKDIOFGSQIKYSCPKGRLIGSSSANTCIISGNTVIMDKTPVCD 154  
+ +G+ +C +G+RL G S++ C++G +W++ P+C+

Sbjct: 1723 VLPPLNLQAKVSVDCDEGRKLGASHCVLQAKMALNSVFPCE 1770

Score = 48.0 bits (112), Expect = 5e-05  
Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)

Query: 26 LLSFSQDCNVPEMLPPARPNTLTDPEPIGTLYNTECRPGYSGR-PFSITCL 79  
L+ S S D C P PF ++ D +F G+ +NY C G+ G P S CL  
Sbjct: 1443 LMSVSEVDCRKRSCGPPPEFNGVHINTDPOF--GSTVNSCDEGRFLIGSP-STTCL 1499

Query: 80 ---KSNWTSADKCRKSCRNPDVNGMAHVIKDIOF--GSOIKYSCPKG-----YR 128  
N W W W C+ SC PP NG + F G+ + Y C G +  
Sbjct: 1500 VSGNNTWMDKAPICHIISCPEPTISNGDFSNMNRFSHNTVTVYQCHTQDQELF 1559

Query: 129 LIGSSSANTCIISGNTV-IMDKTPVCDSELK 158  
L+G S C C + V +W + P C S K  
Sbjct: 1560 LVGRSIVCTSKDQYGVWSSPPEICSTNR 1590

Score = 46.5 bits (108), Expect = 1e-04  
Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)

Query: 57 IGTLYNTECRPGYSGRPF--ITCLKNWTSADKCRKSCRNPDVNG-MAHVI 110  
+G +++ C G+ GR S ++ +W S+ C++ C NP +NG  
Sbjct: 1721 LGAKVFCVDEGRFLKAGNSHCYLAAGALMNSVYVEQIFCENPRLALNGRTGPP 1790

Query: 111 KDIOFGSQIKYSCP-----KGYRLIGSSSANTCIISGNTVIMDKTPVCD 154  
DI +G +I Y+C + LIG SS C GN V W + P C+  
Sbjct: 1791 GDIVKEISYACDTPHGRGNTFLIGBSICTSDPQNGV-WSSVAPCE 1841

Score = 43.8 bits (101), Expect = 9e-04  
Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)

Query: 58 GTLYNTECRPGYSGRPFSTICLKNWTSADKCRKSCRNPDVNGMAHVI---KD 112  
G +Y C PGY G+ F I C ++ CR +C P +NG++ + K

Sbjct: 1870 GMTISTYTCDDPGYLLVKGPF-IFCTDQGIWISQLDHYCKEYVNCSPFLF-MNGISKELMKKV 1927

Query: 113 IQGSGQIKYSCPGYRLIGSSSANCIIISGNTVIMDNKTVCSELEKAPL 162

Sbjct: 1928 YRIQGYTLAKCEGDTYLLSGSPWISQCADRR--WDPLAKTCSHAHDALI 1974

Score = 43.8 bits (101), Expect = 9e-04  
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTYIANTECRPGY----SGRPSTIICLKNSVTSADKCKRCKSCRNPDVNG--MAHYIK 111

Sbjct: 124 GSGQIKYSCPGYRLIGSSSANCIIISGNTVIMDNKTVCSELEKAPL 162

Query: 112 DIQSGQIKYSCPGY----YRLIGSSSANCIIISGNTVIMDNKTVC 153

Sbjct: 184 NFHYGSVYTRCNPGSGGRKRVFELVGEPSIYCTSDNDQVIGSGAPQC 232

Score = 43.0 bits (99), Expect = 0.002  
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGYIANTECRPGY--GRPSITIICLKNSV--WTSAKDKCKRCKSCRNPDVNG--MA 107

Sbjct: 570 DIVGSRINISCTGHRILIGSSSANCIIISGNTVIMDNKTVCSELEKAPL 629

Query: 108 HTIKDIQSGQIKYSCPGY----YRLIGSSSANCIIISGNTVIMDNKTVC 153

Sbjct: 630 TNRENFHYGSVYTRCNPGSGGRKRVFELVGEPSIYCTSDNDQVIGSGAPQC 682

Score = 43.0 bits (99), Expect = 0.002  
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGYIANTECRPGY----SGRPSTIICLKNSVTSADKCKRCKSCRNPDVNG--MAHYI 110

Sbjct: 1278 LGAKVDFVCDGQPLKGSASVSHCVLIGKRSVLMNNSVPCQIFCPSPVPLNG 1337

Query: 111 KDIFGSGQIKYSCPGY----KGYRLIGSSSANCIIIS--GNTVIMDNKTVCSELEK 158

Sbjct: 1338 GDIPYKREISYTCDDPHDRGNTFNLIGSSTIRCTSDPDHNGV-WSPARCELSVR 1392

Score = 42.6 bits (98), Expect = 0.002  
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGYIANTECRPGYSGRPSTIICLKNSVTSADKCKRCKSCRNPDVNG--MA 107

Sbjct: 1020 DIQVSRINISCTGHRILIGSSSANCIIISGNTVIMDNKTVCSELEKAPL 1079

Query: 108 HTIKDIQSGQIKYSCPGY----YRLIGSSSANCIIISGNTVIMDNKTVC 153

Sbjct: 1080 TNRENFHYGSVYTRCNPGSGGRKRVFELVGEPSIYCTSDNDQVIGSGAPQC 1132

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGYIANTECRPGY----SGRPSTIICLKNSVTSADKCKRCKSCRNPDVNGMAHYIKD 112

Sbjct: 378 LGAKVDFVCDGQPLKGSASVSHCVLIGKRSVLMNNSVPCQIFCPSPVPLNG-RHTKXP 436

Query: 113 IQ--FGSGQIKYSCPGY----KGYRLIGSSSANCIIIS--GNTVIMDNKTVC 153

Sbjct: 437 LEVFPGRKAVNYTCDDPHDRGNTFNLIGSSTIRCTSDPDHNGV-WSPARAC 487

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGYIANTECRPGY----SGRPSTIICLKNSVTSADKCKRCKSCRNPDVNGMAHYIKD 112

Sbjct: 828 LGAKVDFVCDGQPLKGSASVSHCVLIGKRSVLMNNSVPCQIFCPSPVPLNG-RHTKXP 886

Query: 113 IQ--FGSGQIKYSCPGY----KGYRLIGSSSANCIIIS--GNTVIMDNKTVC 153

Sbjct: 887 LEVFPGRKAVNYTCDDPHDRGNTFNLIGSSTIRCTSDPDHNGV-WSPARAC 937

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFPARPNLTDPF-----EPIGYIANTECRPGYSGRPSTIICLKN-- 81

Sbjct: 614 IPGGLP--PTIANGDFISTNRENFHYGSVYTRCNPGSGGRKRVFELVGEPSIYCTSDND 670

Query: 82 --SWTSADKCKRCKSCRNPDVNGMAHYIKD---IQGSGQIKYSCPGYRLIGSSSA 135

Sbjct: 671 QVGIMSGAPQCIIIPKCTPPNVENGI--LVSNDRLSFLSINVEVFCQPGYVMGRRV 728

Query: 136 TCIIISGNTVIMDNKTVC 153

Sbjct: 729 KQALNR--WEPELPSC 743

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFPARPNLTDPF-----EPIGYIANTECRPGYSGRPSTIICLKN-- 81

Sbjct: 164 IPGGLP--PTIANGDFISTNRENFHYGSVYTRCNPGSGGRKRVFELVGEPSIYCTSDND 220

Query: 82 --SWTSADKCKRCKSCRNPDVNGMAHYIKD---IQGSGQIKYSCPGYRLIGSSSA 135

Sbjct: 221 QVGIMSGAPQCIIIPKCTPPNVENGI--LVSNDRLSFLSINVEVFCQPGYVMGRRV 278

Query: 136 TCIIISGNTVIMDNKTVC 153

Sbjct: 279 KQALNR--WEPELPSC 293

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPIGYIANTECRPGYSGRPSTIICLKNSVTSADKCKRCKSCRNPDVNG--MA 107

Sbjct: 1792 DIPYKREISYTCDDPHDRGNTFNLIGSSTIRCTSDPDHNGV-WSPARCELSVR 1851

Query: 100 PDPVNG--MAHYIKDIQSGQIKYSCPGYRLIGSSSANCIIISGNTVIMDNKTVC 153

Sbjct: 1852 FRIQNGHYIGVSLYLP--GMTISTYTCDDPGYLLVKGPFIFCTDQ--IMSOLDHYC 1904

Score = 36.7 bits (83), Expect = 0.12  
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PNLTDPF-----EPIGYIANTECRPGYSGRPSTIICLKN--SWTSADK 88

Sbjct: 1523 PLSNGPYSNNRYSFHNQVYVYTCCHGSDGQLFELVGERISITYSKDOQGVMSWSP 1582

Query: 89 DRCKRSCNPPDPVNGMAHVIKIDQSGO---IKYSCPGRYLIGSSSANTCIISGNTVI 145  
+C + P+ N + V + F S I++ C G+ ++G + C + G  
Sbjct: 1583 PRGISTNCTA PEVENAI -RVGNRSFSLTETIRFCQSGVAVGSHVQCQNGR--- 1638

Query: 146 WDKKTPVC 153  
M K P C  
Sbjct: 1639 WGRFLPHC 1646

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPNLTDDFEPIGYLYNECRPGYS-GRPSII-----CLK---NSV 83  
C P + P R T + P P G +NY C P G P + I C N V  
Sbjct: 421 CSPSPVIVBNRHTGKPLEV-FPGKAVNYCDDPHDRGTSFDLIGSTIRCTDPOGNGV 479

Query: 84 WTSADCKR-RKSCNPPDPVNGMAH---IKIDQSGQIKYSCPGRYLIGSSSANTCI 139  
W+S +C C+ P + D G+NY C Y S TC+  
Sbjct: 480 WSSPAFCGILGCOAIPHFLPAKIKTQTNASDPFGISLKYCRPEY-YGRPSITCL- 537

Query: 140 SGNVTYIMDKTPVC 153  
+ ++W + VC  
Sbjct: 538 --DNLWSSPRDVC 549

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPNLTDDFEPIGYLYNECRPGYS-GRPSII-----CLK---NSV 83  
C P + P R T + P P G +NY C P G P + I C N V  
Sbjct: 871 CSPSPVIVBNRHTGKPLEV-FPGKAVNYCDDPHDRGTSFDLIGSTIRCTDPOGNGV 929

Query: 84 WTSADCKR-RKSCNPPDPVNGMAH---IKIDQSGQIKYSCPGRYLIGSSSANTCI 139  
W+S +C C+ P + D G+NY C Y S TC+  
Sbjct: 930 WSSPAFCGILGCOAIPHFLPAKIKTQTNASDPFGISLKYCRPEY-YGRPSITCL- 987

Query: 140 SGNVTYIMDKTPVC 153  
+ ++W + VC  
Sbjct: 988 --DNLWSSPRDVC 999

>GSEQ:AAW71147 Amino acid sequence of the soluble complement  
receptor 1 (sCR1).  
Length = 778

Score = 256 bits (647), Expect = 8e-68  
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLAALVLLLSFS-DQCNVPEMLPFARPNLTDDFEPIGYLYNECRPGYSGRPSI 76  
G LLA -VLL + QCN PEMLPFARPNLTDDFEPIGYLYNECRPGYSGRPSI 89

Query: 30 GLLAVVLLALVAVMGQNAPEMLPFARPNLTDDFEPIGYLYNECRPGYSGRPSI 89

Query: 77 ICLKNSWTSADCKR-RKSCNPPDPVNGMAHVIKIDQSGQIKYSCPGRYLIGSSSANT 136  
ICLKNSWTF AKD+C+RKSCNPPDPVNGM HVIK IQGSGQIKYSC KGYRLIGSSSAT  
Sbjct: 90 ICLKNSWTSADCKR-RKSCNPPDPVNGMAHVIKIQGSGQIKYSCGYRLIGSSSAT 149

Query: 137 CIISGTYIMDKTPVC 154  
CIISG+TYIMDK+TP+CD  
Sbjct: 150 CIISGTYIMDKTPVC 167

Score = 164 bits (412), Expect = 3e-40  
Identities = 74/119 (62%), Positives = 84/119 (70%)  
Query: 35 CNVPEMLPFARPNLTDDFEPIGYLYNECRPGYSGRPSIICLKNSWTSADCKR 94

Sbjct: 498 COADPHFLPAKIKTQTNASDPFGISLKYCRPEYGRYGRPSITCLDNLWSSPRDVC 557  
C P+ FA+ T+ +FPIG L YECR Y GRPSI CL N V+S KD CKR

Query: 95 SCRNPPDPVNGMAHVIKIDQSGQIKYSCPGRYLIGSSSANTCIISGNTVIIMDKTPVC 153  
SC+ PDPVNGM HVI DIQ GS+I YSC G+RLG SSA CI+SGN W R P+C  
Sbjct: 558 SCRTDPVNGMAHVIKIDQSGRINYSCTGHRILIGSSSANTCIISGNTVIIMDKTPVC 616

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSPFDQCNVPEMLPFARPNLTDDFEPIGYLYNECRPGYSGR-PSIICLKNSWTS 86  
L S S C P + A T D F G + Y C PGR R S+ C W+  
Sbjct: 295 LPSCSRVCPDPDVLHARTQDKD-WFSQGVYFSCFEGDVLGAASRRCPDQDMS 353

Query: 87 AKDKRCKRN-PPDPVNGMAHVIKIDQSGQIKYSCPGRYLIGSSSANTCIISGNTVI 145  
A C+ KSC +NG +Q G+++ + C +G+L GSS+ C++G +  
Sbjct: 354 AAFPCEVSCDDFQGLNGRVLPVNLQIAKVDVPCDEGRLKSSASVYLAGMSL 413

Query: 146 WDKKTPVC 154  
M++ PWC+  
Sbjct: 414 WSSSVPC 422

Score = 43.8 bits (101), Expect = 9e-04  
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GYLVYNECRPGY---SGRPSIICLKNSWTSADCKRSCNPPDPVNG--MAHVIK 111  
G+ + Y C GY S II +W + C R C P NG ++ +  
Sbjct: 129 GSGIKYSCRYLIGSSSANTCIISGNTVIIMDKTPVC1PGLPPTIANGDFIS 188

Query: 112 DIQSGQIKYSCPGK-----YRLIGSSSANTCIISGNTV-IMDKTPVC 153  
+GS + Y C G +L+G S C + + V IW P C  
Sbjct: 189 NFHYGSVYTRCNPDSGRKVELWESPTYSNDQVGLMSGRAPOC 237

Score = 43.0 bits (99), Expect = 0.002  
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGYLYNECRPGYS-GRPSIICLKNSV--WTSADCKRSCNPPDPVNG--MA 107  
+G+ +NY C G+ G + L + W++ C-R C P NG ++  
Sbjct: 575 DIQGSRLNYSCTGHRILIGSSSANTCIISGNTVIIMDKTPVC1PGLPPTIANGDFIS 634

Query: 108 HVIKIDQSGQIKYSCPKG-----YRLIGSSSANTCIISGNTV-IMDKTPVC 153  
++ +GS + Y C G +L+G S C + + V IW P C  
Sbjct: 635 TNRENFHYGSVYTRCNPDSGRKVELWESPTYSNDQVGLMSGRAPOC 687

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGYLYNECRPGY-----SGRPSIICLKNSWTSADCKRSCNPPDPVNGMAHVIKID 112  
+G + +C G+ S + + S+W S+ C++ C +PP NG H K  
Sbjct: 383 LKAVYCDDEGFLKSSASVYLAGMSLWSSVPCQICPSPVING-RHTKP 441

Query: 113 IQ---FGSQIKYSCP-----KGYRLIGSSSANTCI--SGNTYIMDKTPVC 153  
++ FG + Y+C +LIG S+ C GN V W + P C  
Sbjct: 442 LEVFPKAVNYCDDPHDRGTSFDLIGSTIRCTDPOGNGV-WSSPAFC 492

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)  
Query: 37 VERNLPFARPNLTDDFEPIGYLYNECRPGYSGRPF-----STICLN-- 81  
+P LP FT DF F G+ + Y C PG GR ST C N



Subject: 169 IPGGLP---PTIINQDPISTNRBNFHYGSVTVYVNCNPGSGKXVFLVYELVPSITVCTSDND 225  
Query: 82 --SWTSAKDKCKRKSCNNPPDPVNGMAHVTKD---IQFGSQIKYSCPKGYRLIGSSSA 135  
+ + + C  
+ + C + P + NG + + D + + + C G + + G  
Subject: 226 QVGIWNGAPQCIIPNKCTPPNVENGI--LVSDNRSLFSLNVEVFCQKPGVVKGRPRV 283  
Query: 136 TCTIISGNTVIMDKRTPVC 153  
C  
W + P C  
Subject: 284 KCOALNK---WEPELPSC 298

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFAFPATNLTDPEFPIGTLYANECRPGYSGRPF-----SIICLNK-- 81  
+ P LP PT DF F G + Y C PG GR SI C N  
Subject: 619 IPGGLP---PTIINQDPISTNRBNFHYGSVTVYVNCNPGSGKXVFLVYELVPSITVCTSDND 675  
Query: 82 --SWTSAKDKCKRKSCNNPPDPVNGMAHVTKD---IQFGSQIKYSCPKGYRLIGSSSA 135  
+ + + C  
+ + C + P + NG + + D + + + C G + + G  
Subject: 676 QVGIWNGAPQCIIPNKCTPPNVENGI--LVSDNRSLFSLNVEVFCQKPGVVKGRPRV 733  
Query: 136 TCTIISGNTVIMDKRTPVC 153  
C  
W + P C  
Subject: 734 KCOALNK---WEPELPSC 748

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFAFPATNLTDPEFPIGTLYANECRPGYSGRPF-----SIICLNK-- 83  
C P + P R T + P P G + NY G + + T C N V  
Subject: 426 CPEPPIVNGRHRGKALEY--FPGKAVNTCTDPHEDRGISFDLIGSTRICTSDPQNGV 484  
Query: 84 WTSANDKCK--RKSCNNPPDPVNGMAHV--IKDIQFGSQIKYSCPKGYRLIGSSSA 139  
W+S + C C + P + D G + XY C Y S TC+  
Subject: 485 WSSPAFRGILGHGQAFHFLAKTYQNASDPPIGTSIAKYECRPRY--YGRPFSTCL-- 542  
Query: 140 SGNVTIWMNKTPVC 153  
+ + W + VC  
Subject: 543 --DNLMWSSPRDYC 554

>GSEQ:MAR11810 Human complement type 1 receptor.  
Length = 2039

Score = 256 bits (647), Expect = 8e-68  
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLLAALVLLISFS--DQCNPEMLPFAFPATNLTDPEFPIGTLYANECRPGYSGRPF 76  
G LLA +VLL + QCN PEMLPFAFPATNLTD+PEPPIGTLYANECRPGYSGRPF  
Subject: 25 GSLAVVLLALPVAMGQCNAPMLPFAFPATNLTDPEFPIGTLYANECRPGYSGRPF 84  
Query: 77 ICLKNSVWTSKDKCKRKSCNNPPDPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSA 136  
ICLKNSVWTF AKD+C+RKSCNNPPDPVNGM HVK IQFGSQIYSC KGYRLIGSSSA  
Subject: 85 ICLKNSVWTSKDKCKRKSCNNPPDPVNGMAHVTKIQFGSQIKYSCGYRLIGSSSA 144  
Query: 137 CIISGNTVIMDKRTPVC 154  
CIISG+TVIMDN+TP+CD  
Subject: 145 CIISGNTVIMDKRTPVC 162

Score = 176 bits (442), Expect = 9e-44  
Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSPDCQNPPEMLPFAFPATNLTDPEFPIGTLYANECRPGYSGRPF-----SIICLNKSWTS 87  
LS + C PE PPA PT +PEP+GT LNERGRGY GA PSI CLN VM+S  
Subject: 1389 LSVNAGCKTPEQPFASPTIINDFERVIGSLNIEGRGTYGRTISCLNLMWSSV 1448  
Query: 88 KDKCKRKSCNNPPDPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSA 147  
+D+K+RSC PP+P NGM H+ D QFGS + YSC +G+RLIGS S TC++SGN V WD  
Subject: 1449 EDNCRKRSQGPPEPFGMAHVINTDQFGSTVNSCNEGRFLIGSPSTCLVSGNNVTMD 1508  
Query: 148 NKRTFVCD 154  
K P+C+  
Subject: 1509 KKAPICE 1515

Score = 166 bits (417), Expect = 8e-41  
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 CNVPEMLPFAFPATNLTDPEFPIGTLYANECRPGYSGRPF-----SIICLNKSWTS 94  
C P + PA + T + +PEP+GT L YECRP Y GRPFI CL N VM+S KD CKR  
Subject: 943 COADPHFLAKLQVNAADPFIQTSIAKYECRPRYGRPFSTICLNLVWSSPRDYC 1002  
Query: 95 SCNNPPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSA 153  
SC+ PDPVNGM HVY DIQ GS+I YSC +G+RLIG SSA CI+SGN W R P+C  
Subject: 1003 SKCTPPDPVNGMAHVTKDIQVGSRIINISCTTGRHLIGSSAECILSGNTAHWSTKPPIC 1061

Score = 164 bits (412), Expect = 3e-40  
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVPEMLPFAFPATNLTDPEFPIGTLYANECRPGYSGRPF-----SIICLNKSWTS 94  
C P + PA + T + +PEP+GT L YECRP Y GRPFI CL N VM+S KD CKR  
Subject: 493 COADPHFLAKLQVNAADPFIQTSIAKYECRPRYGRPFSTICLNLVWSSPRDYC 552  
Query: 95 SCNNPPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSA 153  
SC+ PDPVNGM HVY DIQ GS+I YSC +G+RLIG SSA CI+SGN W R P+C  
Subject: 553 SKCTPPDPVNGMAHVTKDIQVGSRIINISCTTGRHLIGSSAECILSGNTAHWSTKPPIC 611

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSPDCQNPPEMLPFAFPATNLTDPEFPIGTLYANECRPGYSGRPF-----SIICLNKSWTS 86  
L S S C P + A T D F G + Y C PGT R S + C W+  
Subject: 740 LPSCSRVQDPEPVLHAKRTQDKD--NFSPOQEVYFSCPEGIDLGMAASNRCTPQGMSP 798  
Query: 87 AKDKCKRKSCNN--PDPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSA 145  
A C + KSC + +NG + +Q G + + + C +G+ +L GSS+ + C + + + G +  
Subject: 799 AAPTEVNSCDDPMQQLNGRVLPVNIQLGAKVDCDEGFLKSSASVYCVLAGMESL 858  
Query: 146 WDNKTPVCD 154  
W++ P+C+  
Subject: 859 WNSVFPCE 867

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSPDCQNPPEMLPFAFPATNLTDPEFPIGTLYANECRPGYSGRPF-----SIICLNKSWTS 86  
L S S C P + A T D F G + Y C PGT R S + C W+  
Subject: 290 LPSCSRVQDPEPVLHAKRTQDKD--NFSPOQEVYFSCPEGIDLGMAASNRCTPQGMSP 348  
Query: 87 AKDKCKRKSCNN--PDPVNGMAHVTKDIQFGSQIKYSCPKGYRLIGSSSA 145  
A C + KSC + +NG + +Q G + + + C +G+ +L GSS+ + C + + + G +  
Subject: 349 AAPTEVNSCDDPMQQLNGRVLPVNIQLGAKVDCDEGFLKSSASVYCVLAGMESL 408  
Query: 146 WDNKTPVCD 154

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

5/5/03 8:58 PM

5/5/03 8:58 PM

Score = 41.4 bits (95), Expect = 0.005  
 Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTALTECRPGY-----SGRPSITCLKNSVTSKDKCRKCRNPDPVNGMAHYID 112  
 +G +++ C G+ S ++ S+W S+ C++ C +PP NG H R  
 Sbjct: 828 LQAKVDVCDGQKSSASVCLAGSLNWSVPCQJFCSPVPLENG-RHNGRP 886

Query: 113 IQ---FSGQIKYSCP-----KGYRLIGSSSACII--SGNTVINDKRTVPC 153  
 ++ PG + Y+C + Lig S+ C GN V W + P C  
 Sbjct: 887 LEVFPFGKAVNYTCDPHEDRGTSFDLIGESTRICTSDPQNGV-WSSPAPRC 937

Score = 37.5 bits (85), Expect = 0.067  
 Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPENLPFAPRPNTLDDF-----EPPIGTALTECRPGYSGRPF-----SIICLN-- 81  
 +P LP PT DF F G+ + Y C PG GR SI C N  
 Sbjct: 614 IPGGLP---PTIANGDFISTNENHFGSVVYTRCNGSGKRPVELGPEPSIYCTSDND 670

Query: 82 --SVWTSKDKCRKCRNPDPVNGMAHYID---IQFGSQIKYSCPKGYRLIGSSSA 135  
 +W+ +C + PP NG+ ++ D ++ C G+ + G  
 Sbjct: 671 QVGIWSPAPQCIIPNCKTPEVNGI--LVSDNNSLFLSINEVVEFGQPGVNGGRNV 728

Query: 136 TCIISGNTVINDKRTVPC 153  
 C W+ + P C  
 Sbjct: 729 KQALNR---WEPELPSC 743

Score = 37.5 bits (85), Expect = 0.067  
 Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPPIGTYLMECRPGYS-GRPSII-----CLK-----NSWTSKDKCRK--SCRP 99  
 +P G +Y+C G P+I C N WWS+ C+P  
 Sbjct: 1792 DLPFGKELIYACDHPGRGATPNDIGESINCTSDPQNGWSSPAPRCLEISVPAACRPF 1851

Query: 100 PDPVNGM--AHVTKDIQFGSQIKYSCPKGYRLIGSSSACIIISGNTVINDKRTVPC 153  
 P NG HV + G I Y+C GY L+G C G IW C  
 Sbjct: 1852 PRLONGHYIGHVSILYLP-GMTISYTCDDPYLLVKGPIFCTDQ--IWSQLDHYC 1904

Score = 36.7 bits (83), Expect = 0.12  
 Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 PTNLTDDF-----EPPIGTALTECRPGYSGRPF-----SIICLN--SVWTSK 88  
 PF DF F GT + Y+C G G SI C VW+S  
 Sbjct: 1523 PTIANGDFISTNENHFGSVVYTRCNGSGKRPVELGPEPSIYCTSDNDVSSP 1582

Query: 89 DCKRKSCHNPDPVNGMAHYIDIQFGSQ--IKYSCPKGYRLIGSSSACIIISGNTV 145  
 +C + P+ N + V + P S I++ C G+ ++GS + C +G  
 Sbjct: 1583 PRCISTNKTCAEVENAI-RVNGRSPFSLTEIRFCQPGFVWVSGHTVCCQTNGR-- 1638

Query: 146 WDKRTVPC 153  
 W K P C  
 Sbjct: 1639 WGRPLPHC 1646

Score = 34.0 bits (76), Expect = 0.76  
 Identities = 32/138 (23%), Positives = 50/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPENLPFAPRPNTLDDF-----EPPIGTALTECRPGYSGRPF-----SIICLN-- 81  
 +P LP PT DF F G+ + Y C PG GR SI C N  
 Sbjct: 164 IRGGLP---PTIANGDFISTNENHFGSVVYTRCNGSGKRPVELGPEPSIYCTSDND 220

Query: 82 --SVWTSKDKCRKCRNPDPVNGMAHYID---IQFGSQIKYSCPKGYRLIGSSSA 135  
 +W+ +C + PP NG+ ++ D ++ C G+ + G  
 Sbjct: 221 QVGIWSPAPQCIIPNCKTPEVNGI--LVSDNNSLFLSINEVVEFGQPGVNGGRNV 278

Query: 136 TCIISGNTVINDKRTVPC 153  
 C W+ + P C  
 Sbjct: 279 KQALNR---WEPELPSC 293

Score = 32.8 bits (73), Expect = 1.7  
 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPAPRPNTLDDFEPPIGTALTECRPGYS-GRPSII-----CLK-----NSV 83  
 C P +P R T + PP G+ +Y C P G P +I C N V  
 Sbjct: 421 CSPPVIENRHRNGRPLEV-FPGGAVNYTCDPHEDRGTSFDLIGESTRICTSDPQNGV 479

Query: 84 WTSKDKCRKCRNPDPVNGMAHYID---IQFGSQIKYSCPKGYRLIGSSSACII 139  
 W+S +C C+ P + D G+ +KY C Y S TC+  
 Sbjct: 480 WSSPAPRCGILGHCOAPDHPFLAKLQYMASDPFGISLAKYCRPEY-YGRPFSTCL- 537

Query: 140 SGNTVINDKRTVPC 153  
 + ++W + VC  
 Sbjct: 538 --DNLWMSFPDVC 549

Score = 32.8 bits (73), Expect = 1.7  
 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPAPRPNTLDDFEPPIGTALTECRPGYS-GRPSII-----CLK-----NSV 83  
 C P +P R T + PP G+ +Y C P G P +I C N V  
 Sbjct: 871 CSPPVIENRHRNGRPLEV-FPGGAVNYTCDPHEDRGTSFDLIGESTRICTSDPQNGV 929

Query: 84 WTSKDKCRKCRNPDPVNGMAHYID---IQFGSQIKYSCPKGYRLIGSSSACII 139  
 W+S +C C+ P + D G+ +KY C Y S TC+  
 Sbjct: 930 WSSPAPRCGILGHCOAPDHPFLAKLQYMASDPFGISLAKYCRPEY-YGRPFSTCL- 987

Query: 140 SGNTVINDKRTVPC 153  
 + ++W + VC  
 Sbjct: 988 --DNLWMSFPDVC 999

>GSDQ:ABP92219 CR1 protein.  
 Length = 2317

Score = 256 bits (647), Expect = 8e-68  
 Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)

Query: 18 GLDLAALTLSSFS-DOCVNPEMLPAPRPNTLDDFEPPIGTALTECRPGYSGRPSI 76  
 G LLA +VIL + QCN PEMLPAPRPNTLDDFEPPIGTALTECRPGYSGRPSI 93  
 Sbjct: 34 GSLAVVLLALFVAMGQCNAPMLPAPRPNTLDDFEPPIGTALTECRPGYSGRPSI 93

Query: 77 ICLKNSVWTSKDKCRKCRNPDPVNGMAHYIDIQFGSQIKYSCPKGYRLIGSSSAT 136  
 ICLKNSVWTSKDKCRKCRNPDPVNGMAHYIDIQFGSQIKYSCPKGYRLIGSSSAT 153  
 Sbjct: 94 ICLKNSVWTSKDKCRKCRNPDPVNGMAHYIDIQFGSQIKYSCPKGYRLIGSSSAT 153

Query: 137 CIISGNTVINDKRTVPC 154  
 CIISG+TVINDN+TP+CD  
 Sbjct: 154 CIISGNTVINDKRTVPC 171

Score = 176 bits (442), Expect = 9e-44  
 Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSSDQCNVPEMLPAPRPNTLDDFEPPIGTALTECRPGYSGRPSIICLKNSWTS 87  
 LS + C PE PPA PT +DPEP+GT LNECHRGY G+ FSI CLK+ VW+S

Sbjct: 1398 LSVAGHCKTEBPFPASPTTIPINDEFVVGSTLNTECRPGYFGKMFSTICLENLWMSV 1457  
Query: 88 KDKCKRSKRNPPDPVNGAHVINDIOPGSOIKYSCPKGRLIGSSSANTCIISGNTVMD 147  
+D+KRSK PP+P NGM H+ D QFGS + YSC +G+RLIGS S TC++SGN V MD  
Sbjct: 1458 EDNCRKRSKGPPEFNGVHINTDQFGSTVNSCNEGRLIGSBSPTCLVSGNNVMD 1517  
Query: 148 NKRTVCD 154  
K P+C+  
Sbjct: 1518 KKAPICR 1524  
Score = 166 bits (417), Expect = 8e-41  
Identities = 75/119 (63%), Positives = 85/119 (71%)  
Query: 35 C NVEPMLPPARPNTLNDDEFPPIGYLVNTECRPGYSGRPSTICLNKNSVTSADCKRK 94  
C P+ FA+ T+ +PPIGT L YECRP Y GRPST CL N VM+S KD CKR  
Sbjct: 952 CQADPHLFAKLTQTNASDPPIGTSLKRECPYGRPSTICLNKNSVTSADCKRK 1011  
Query: 95 SCRPDPVNGAHVINDIOPGSOIKYSCPKGRLIGSSSANTCIISGNTVMDNKTPVC 153  
SC+ PDPVNGM HVI DIQ GS+I YSC G+RLIG SSA CI+SGN W K P+C  
Sbjct: 1012 SCRTPEPVGNGVHINTDQFGSTVNSCTGRLIGSSSANTCIISGNTVMDNKTPVC 1070  
Score = 164 bits (412), Expect = 3e-40  
Identities = 74/119 (62%), Positives = 84/119 (70%)  
Query: 35 C NVEPMLPPARPNTLNDDEFPPIGYLVNTECRPGYSGRPSTICLNKNSVTSADCKRK 94  
C P+ FA+ T+ +PPIGT L YECRP Y GRPST CL N VM+S KD CKR  
Sbjct: 502 CQADPHLFAKLTQTNASDPPIGTSLKRECPYGRPSTICLNKNSVTSADCKRK 561  
Query: 95 SCRPDPVNGAHVINDIOPGSOIKYSCPKGRLIGSSSANTCIISGNTVMDNKTPVC 153  
SC+ PDPVNGM HVI DIQ GS+I YSC G+RLIG SSA CI+SGN W K P+C  
Sbjct: 562 SCRTPEPVGNGVHINTDQFGSTVNSCTGRLIGSSSANTCIISGNTVMDNKTPVC 620  
Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)  
Query: 28 LLSFSDQCVNPEMLPPARPNTLNDDEFPPIGYLVNTECRPGYSGR-PFSTICLNKNSVTS 86  
L S S C P + A T D P G + Y C PGY R S+C W+  
Sbjct: 749 LPSCSRVCOPEPVLHAKRTQDKD-NFSQGEVYSCPEGDLRGAASNRCTQGDWSP 807  
Query: 87 AKDKRKRSKRN-PPDPVNGAHVINDIOPGSOIKYSCPKGRLIGSSSANTCIISGNTV 145  
A C+ KSC + +NG ++Q G+++ + C +G+L GSS++ C+++ +  
Sbjct: 808 AAPCEVYSCDPPMGQLNGRVLPVNLQAKVDVFCDEGQLKSSASVCLAGMESL 867  
Query: 146 WDKTPVCD 154  
W++ PVC+  
Sbjct: 868 WNSVPCVCE 876  
Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)  
Query: 28 LLSFSDQCVNPEMLPPARPNTLNDDEFPPIGYLVNTECRPGYSGR-PFSTICLNKNSVTS 86  
L S S C P + A T D P G + Y C PGY R S+C W+  
Sbjct: 299 LPSCSRVCOPEPVLHAKRTQDKD-NFSQGEVYSCPEGDLRGAASNRCTQGDWSP 357  
Query: 87 AKDKRKRSKRN-PPDPVNGAHVINDIOPGSOIKYSCPKGRLIGSSSANTCIISGNTV 145  
A C+ KSC + +NG ++Q G+++ + C +G+L GSS++ C+++ +  
Sbjct: 358 AAPCEVYSCDPPMGQLNGRVLPVNLQAKVDVFCDEGQLKSSASVCLAGMESL 417  
Query: 146 WDKTPVCD 154  
W++ PVC+  
Sbjct: 418 WNSVPCVCE 426

Score = 64.8 bits (155), Expect = 4e-10  
Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)  
Query: 28 LLSFSDQCVNPEMLPPARPNTLNDDEFPPIGYLVNTECRPGYSGR-PFSTICLNKNSVTS 86  
L S S C P + A T D P G + Y C PGY R S+C W+  
Sbjct: 1199 LPSCSRVCOPEPVLHAKRTQDKD-NFSQGEVYSCPEGDLRGAASNRCTQGDWSP 1257  
Query: 87 AKDKRKRSKRN-PPDPVNGAHVINDIOPGSOIKYSCPKGRLIGSSSANTCIISGNTV 145  
+C KSC + +NG ++Q G+++ + C +G+L GSS + C++ G +  
Sbjct: 1258 BAPRCVAKSCDPLQGLPHGRVLPVNLQAKVDVFCDEGQLKSSASVCLVGMESL 1317  
Query: 146 WDKTPVCD 154  
W+N PVC+  
Sbjct: 1318 WNSVPCVCE 1326  
Score = 61.3 bits (146), Expect = 5e-09  
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)  
Query: 49 LDDPEPPIGYLVNTECRPGYSGR-PFSTICLNKNSVTSADCKRKSNPPDPV-NGM 106  
L+ F G + Y C P Y R S+C W+ +C KSC + +G  
Sbjct: 1672 LSHODNFSQGEVYSCPESTDLGASLHCTQGDWSPBAPRCVAKSCDPLQGLPHGR 1731  
Query: 107 AHVINDIOPGSOIKYSCPKGRLIGSSSANTCIISGNTVMDNKTPVC 154  
+ ++Q G+++ + C +G+RL G S++ C+++ +W++ PVC+  
Sbjct: 1732 VLLPVLNQLGAKVSVFCDEGRLKGRSASHCVLAKMALWNSVPCVCE 1779  
Score = 48.0 bits (112), Expect = 5e-05  
Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)  
Query: 26 LLSFSDQCVNPEMLPPARPNTLNDDEFPPIGYLVNTECRPGYSGR-PFSTICLNKNSVTS 79  
L+ S S D C P PF ++ D +F G+ +NY C G+ G P S CL  
Sbjct: 1452 LMSVENDKCRKSCGPEPFGVNGVHINTVDF--GSTVYSCNEGRLIGSP-STYCL 1508  
Query: 80 ---NNSVTSADCKRKSNPPDPVNGAHVINDIOPGSOIKYSCPKGRLIGSSSANTCIISGNTV 128  
N W C+ SC PP NG + F G+ + Y C G  
Sbjct: 1509 VSGNNVYMDKAPICELISCEPPTISNGDVSNNRSTFNGVTVYQCHTQDGBOLFE 1568  
Query: 129 LIGSSSANTCIISGNTV-INDKTPVCDSELK 158  
L+G S C + V +W + P C S K  
Sbjct: 1569 LVGRSIVCTSKDQVGVWSSPPRCISTNRK 1599  
Score = 46.5 bits (108), Expect = 1e-04  
Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)  
Query: 57 IGTVLNTECRPGY--SGRPFS--IICLNKNSVTSADCKRKSCNPPDPVNG--MAHVI 110  
+G +++ C G+ GR S ++ ++W S+ C++ C NRP +NG  
Sbjct: 1740 LGANVFPVCDGPRFKGRSASHCVLAKMALWNSVPCVQGIQCPNPFPALINRHTGPP 1799  
Query: 111 KDIOGSOIKYSCP-----KGRALIGSSSANTCIISGNTVMDNKTPVC 154  
DI +G +I Y+C + LIG SS C GN V W + P C +  
Sbjct: 1800 GDIVYKREIYACDHPDRGNTVNLIGSSSIRCTSDPQANV-WSSPAPCE 1650  
Score = 43.8 bits (101), Expect = 9e-04  
Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)  
Query: 58 GTVLNTECRPGY--GRPSTICLNKNSVTSADCKRKSCNPPDPVNGAHVIT--KD 112  
G +Y C PGY G+ P I C +W+ CK +C P +NG++ + K  
Sbjct: 1879 GMTISTCTDPPGVLLVQKGP-IFCTDQIGMSQDLHCKREVNCSPLP-INGISRELMKTV 1936

Query: 113 IQFGSQRKSCPRGYRLIGSSATCIIISGNTVIMDKKTPVCDSEKAYFL 162  
+G + C GY L GS + C MD C S A +  
Sbjct: 1937 YHGGDYVTLKCEGDTYLTGSPWQCAADR---WDPLAKCTSHADALI 1983

Score = 43.8 bits (101), Expect = 9e-04  
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GYVLANTECRPGY----SGRPSIICLNKSVWTSADCKRKRSCNRPDPVNG--MAHYIK 111  
+G + Y C GY S II +W + C R C PP NG ++ +  
Sbjct: 133 GSQIKYCTCKGRIIGSSATCIIISGNTVIMDKKTPVCDSEKAYFL 192

Query: 112 DIOFGSQRKSCPRG-----YRLIGSSATCIIISGNTVIMDKKTPVC 153  
+ +GS + Y C G + L+G S C + + V IW P C  
Sbjct: 193 NPHGSVVYTRCNPGSGRKFELVGPSTICTSDPDQGVMSGAPAC 241

Score = 43.0 bits (99), Expect = 0.002  
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTYLANTECRPGYS--GRPSIICLNKSV--WTSADCKRKRSCNRPDPVNG--MA 107  
+ +G + NY C G+ G + L + M+ + C+R C PP NG ++ +  
Sbjct: 579 DIOGSRINYSCTGHRILGHSSACILSGNAHMSKTPICQRIPLGPLEPTIANGDFIS 638

Query: 108 HVIKDIOFGSQRKSCPRG-----YRLIGSSATCIIISGNTVIMDKKTPVC 153  
+ +GS + Y C G + L+G S C + + V IW P C  
Sbjct: 639 TNRBNHYSVYTRCNPGSGRKFELVGPSTICTSDPDQGVMSGAPAC 691

Score = 43.0 bits (99), Expect = 0.002  
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGTVLANTECRPGY----SGRPSIICLNKSVWTSADCKRKRSCNRPDPVNG--MAHYI 110  
+G +++ C G+ S ++ S+W ++ C+ C NP +NG  
Sbjct: 1287 LKAQVYVCDGRLKGSVSHCVLGNBSIMNNSVPCCHICPPRIALINGHCTIS 1346

Query: 111 KDIOFGSQRKSCPRG-----KGRILIGSSATCIIISGNTVIMDKKTPVC 158  
DI +G +I Y+C + LIG S+ C GN V W + P C+ ++  
Sbjct: 1347 GDIPGKEISTYCDHPDRGATFNILGISTRICTSDPDHNGV--WSSPARELSVR 1401

Score = 42.6 bits (98), Expect = 0.002  
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTYLANTECRPGYSRPF-----IICLNKSVWTSADCKRKRSCNRPDPVNG--MA 107  
+ +G + NY C G+ S I+ + W+ + C+R C PP NG ++ +  
Sbjct: 1029 DIOGSRINYSCTGHRILGHSSACILSGNTYHMSKTPICQRIPLGPLEPTIANGDFIS 1088

Query: 108 HVIKDIOFGSQRKSCPRG-----YRLIGSSATCIIISGNTVIMDKKTPVC 153  
++ +GS + Y C G + L+G S C + + V IW P C  
Sbjct: 1089 TNRBNHYSVYTRCNPGSGRKFELVGPSTICTSDPDQGVMSGAPAC 1141

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTVLANTECRPGY----SGRPSIICLNKSVWTSADCKRKRSCNRPDPVNGMAHYIKD 112  
+G +++ C G+ S ++ S+W S+ C+ + C+P NG H K  
Sbjct: 387 LKAQVYVCDGRLKGSASVYCLAGHESIMNNSVPCCHICPPRIALINGHCTIS 445

Query: 113 IQ---FGSQRKSCPRG-----KGRILIGSSATCIIISGNTVIMDKKTPVC 153  
++ ++ FG + Y+C + LIG S+ C GN V W + P C  
Sbjct: 446 LEVFPFGKAVNYTCDHPDRGTSPLIGESTRICTSDPDQGV--WSSPAPRC 496

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTVLANTECRPGY----SGRPSIICLNKSVWTSADCKRKRSCNRPDPVNGMAHYIKD 112  
+G +++ C G+ S ++ S+W S+ C+ + C+P NG H K  
Sbjct: 837 LKAQVYVCDGRLKGSASVYCLAGHESIMNNSVPCCHICPPRIALINGHCTIS 895

Query: 113 IQ---FGSQRKSCPRG-----KGRILIGSSATCIIISGNTVIMDKKTPVC 153  
++ ++ FG + Y+C + LIG S+ C GN V W + P C  
Sbjct: 896 LEVFPFGKAVNYTCDHPDRGTSPLIGESTRICTSDPDQGV--WSSPAPRC 946

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFPARPTNLTDPF-----EPIGTYLANTECRPGYSRPF-----SIICLNK-- 81  
+P LP PP DP F G+ + Y C PG GR SI C N  
Sbjct: 623 IPCGLP---PTIANGDFISTNRBNHYSVYTRCNPGSGRKFELVGPSTICTSDND 679

Query: 82 --SWTSADCKRKRSCNRPDPVNGMAHYIKD---IQFGSQRKSCPRGRLIGSSA 135  
+W+ +C + PP+ NG+ ++ D +++ C G+ + G  
Sbjct: 680 QVGWISGAPQCIIIPKCTPPVWENGI--LVSDNRSLFSLNEVVEFRCOPGVKGRPV 737

Query: 136 TCIIISGNTVIMDKKTPVC 153  
C W+ + P C  
Sbjct: 738 KCOALNK---WEPELPSC 752

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFPARPTNLTDPF-----EPIGTYLANTECRPGYSRPF-----SIICLNK-- 81  
+P LP PP DP F G+ + Y C PG GR SI C N  
Sbjct: 173 IFCGLP---PTIANGDFISTNRBNHYSVYTRCNPGSGRKFELVGPSTICTSDND 229

Query: 82 --SWTSADCKRKRSCNRPDPVNGMAHYIKD---IQFGSQRKSCPRGRLIGSSA 135  
+W+ +C + PP+ NG+ ++ D +++ C G+ + G  
Sbjct: 230 QVGWISGAPQCIIIPKCTPPVWENGI--LVSDNRSLFSLNEVVEFRCOPGVKGRPV 287

Query: 136 TCIIISGNTVIMDKKTPVC 153  
C W+ + P C  
Sbjct: 288 KCOALNK---WEPELPSC 302

Score = 37.5 bits (85), Expect = 0.067  
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPIGTYLANTECRPGYS--GRPSIICLNKSVWTSADCKRKRSCNRPDPVNG--MAHYI 110  
+ P G +Y C G F+I C N VM+S +C+ +C +P  
Sbjct: 1801 DIPGKEISTYCDHPDRGATFNILGISTRICTSDPDQGVMSGAPRCBELSVAPACHP 1860

Query: 100 PDPVNGK---AHVTKDIOFGSQRKSCPRGYRLIGSSATCIIISGNTVIMDKKTPVC 153  
PV NG HV + G I Y+C GY L+G C G IW C  
Sbjct: 1861 RFIQNGHYIGHVSILYLP--GMTISTYCDPDGRLVKGRICTDQG---TWSQDHYC 1913

Score = 36.7 bits (83), Expect = 0.12  
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

Query: 46 FPNLTDPF-----EPIGTYLANTECRPGYSRPF-----SIICLNK---SWTSAK 88  
FP DP F G+ + Y+C G G SI C VM+S  
Sbjct: 1532 PTIANGDFISTNRBNHYSVYTRCNPGSGRKFELVGPSTICTSDPDQGVMSGAPRC 1591

Query: 89 DCKRKRSCNRPDPVNGMAHYIKDIOFGSQ---IKYSGRGRILIGSSATCIIISGNTV 145  
+C + P+ N + V + F S I++ C G+ +GS + C +G

Query: 1592 PRGISTNCTAPREVENAI-RVPGNRSPFSLTETIRFCQGFVWVSHVQCOTNGR--- 1647

Query: 146 WDKRTDVC 153

Query: 1648 WGRFLDVC 1655

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYS-GRPFSII-----CLK---NSV 83

Query: 430 CSPSPVPIPNRHTGKPLEV-FPGKAVNYCDDHPDGTSLDLSRTICTSDPGNGV 488

Query: 84 WTSKDKCK-RKSCNRPDPVNGMAHV---IKDIOFSGQIKYSCRGYRLIGSSSANTCI 139

Query: 489 WSSPAPFCGLGHQADPHFLPAKLKTQTNASDPFGISLKYCRPEY-YGRPFSITCL- 546

Query: 140 SGNVTIWMKTPVC 153

Query: 547 --DNLWSSPKDVC 558

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYS-GRPFSII-----CLK---NSV 83

Query: 880 CSPSPVPIPNRHTGKPLEV-FPGKAVNYCDDHPDGTSLDLSRTICTSDPGNGV 938

Query: 84 WTSKDKCK-RKSCNRPDPVNGMAHV---IKDIOFSGQIKYSCRGYRLIGSSSANTCI 139

Query: 939 WSSPAPFCGLGHQADPHFLPAKLKTQTNASDPFGISLKYCRPEY-YGRPFSITCL- 996

Query: 140 SGNVTIWMKTPVC 153

Query: 997 --DNLWSSPKDVC 1008

>GSEQ:AA28562 CRI-4 (116K) analogue.  
Length = 543

Score = 253 bits (639), Expect = 7e-67  
Identities = 111/121 (91%), Positives = 116/121 (95%)

Query: 34 OCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPFSIIICLKNSVWTSKDKCKR 93

Query: 1 OCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPFSIIICLKNSVWTSKDKCKR 60

Query: 94 KSCNRPDPVNGMAHVTDIOFSGQIKYSCRGYRLIGSSSANTCIISGVYIWMKTPVC 153

Query: 61 KSCNRPDPVNGMAHVTDIOFSGQIKYSCRGYRLIGSSSANTCIISGVYIWMKTPVC 120

Query: 154 D 154

Query: 121 D 121

Score = 128 bits (319), Expect = 2e-29  
Identities = 38/92 (41%), Positives = 65/92 (70%)

Query: 35 CNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPFSIIICLKNSVWTSKDKCKR 94

Query: 452 COADPHFLPAKLKTQTNASDPFGISLKYCRPEY-YGRPFSITCLDNLWSSPKDVC 511

Query: 95 SCNRPDPVNGMAHVTDIOFSGQIKYSCPKG 126

Query: 512 SCNRPDPVNGMAHVTDIOFSGQIKYSCPKG 543

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSRSQCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPFSIIICLKNSVWTS 86

Query: 249 LPSRSQCNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPFSIIICLKNSVWTS 307

Query: 87 AKDKCKRCKR-PDPVNGMAHVTDIOFSGQIKYSCRGYRLIGSSSANTCIISGVYI 145

Query: 308 AAPCEVSCDDPFGQLNGRVLPVNIOLGAKVDFVCDRQGLKSSASVYLAGMESTL 367

Query: 146 WDKRTDVC 154

Query: 368 WSSVPCVC 376

Score = 43.8 bits (101), Expect = 9e-04  
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GYLYANECRPGY-----SGRPFSIIICLKNSVWTSKDKCKRSCNRPDPVNG-NAHVTK 111

Query: 83 GQIKYSCRGYRLIGSSSANTCIISGVYIWMKTPVCIDRIPGAPITNDGISTJSTRE 142

Query: 112 DIORGQIKYSCPKG-----YRLIGSSSANTCIISGVYIWMKTPVC 153

Query: 143 NHTGSAVTRCNPSGAKRYELVGPSTICTSNDQVQVWNGARPC 191

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGYLYANECRPGY-----SGRPFSIIICLKNSVWTSKDKCKRSCNRPDPVNGMAHVTK 112

Query: 337 LGKAVDFVCDRQGLKSSASVYLAGMESTLWSSVPCVCEQIFCSPVPIBNG-RHTGK 395

Query: 113 IQ-----FGQIKYSCPKG-----YRLIGSSSANTCIISGVYIWMKTPVC 153

Query: 396 LEPVPEKAVNTCDPHDRGTSFDLIGESTRICTSDPGNGV-WSSAPRC 446

Score = 34.0 bits (76), Expect = 0.76  
Identities = 32/138 (23%), Positives = 50/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPFARPTNLTDPEFPIGYLYANECRPGYSGRPFSIIICLKNSVWTSKDKCKR 81

Query: 123 IPGGLP---PTTNDGISTJSTRENAHVYVYRCNPGKRYELVGPSTICTSND 179

Query: 82 --SWTSADCKRCKRSCNRPDPVNGMAHVTDIOFSGQIKYSCPKG--YRLIGSSSANTCI 135

Query: 180 QVWISGAPADPCLINRCPENWENG-LLVSDNRSLSLAEVVERPCQVYVWAKGRPV 237

Query: 136 TCIISGVYIWMKTPVC 153

Query: 238 KQALNR---WEPFLDVC 252

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVPEMLPFARPTNLTDPEFPIGYLYANECRPGYS-GRPFSII-----CLK---NSV 83

Query: 360 CSPSPVITNGHHTGKPLEY-FPPGKAVNYTDDPHDRGTSFDLIGESTIRCTSDPQNGV 438  
+G S C P + P G +NY C P G F +I C N V  
Query: 84 WTSADCKR-RKSCNPPDPVNGMAHV---IKDIQSGQIKYSCPGYRLIGSSSANCII 139  
+S +C C P + D G +RY C Y S TC+  
Query: 439 WSSPAPRGILGHCOAHPDLFAKLQYNASDPPIGTSLKRYCRPEY-YGRPFSITCL- 496  
+ +W + VC  
Query: 140 SGNVYIMDKTPVC 153  
+ +W + VC  
Query: 497 --DNLMWSSPDVVC 508

>GSEQ:AA28552 CRI-4 (78T, 79D) analogue.

Length = 563

Score = 252 bits (636), Expect = 2e-66  
Identities = 110/121 (90%), Positives = 116/121 (94%)

Query: 34 QCNVEMLPAPAPNLTDDEPPIGYIANTBCRPGYSGRPSIICLNKSWTSADCKCR 93  
QCN PEARPPNLTD+PEPPIGYIANTBCRPGYSGRPSIICLNKSWT AKD+C+R  
Query: 1 QCNAPMLPAPAPNLTDDEPPIGYIANTBCRPGYSGRPSIICLNKSWTADCKCR 60  
QCNAPMLPAPAPNLTDDEPPIGYIANTBCRPGYSGRPSIICLNKSWTADCKCR  
Query: 94 KSCNPPDPVNGMAHVIKDIQSGQIKYSCPGYRLIGSSSANCIIISGNVIMDKTPVC 153  
KSCNPPDPVNGMAHV IKDIQSGQIKYSC PGYRLIGSSSANCIIISGNVIMDKTPVC  
Query: 61 KSCNPPDPVNGMAHVIKDIQSGQIKYSCPGYRLIGSSSANCIIISGNVIMDKTPVC 120  
KSCNPPDPVNGMAHV IKDIQSGQIKYSC PGYRLIGSSSANCIIISGNVIMDKTPVC  
Query: 154 D 154  
D  
Query: 121 D 121

Score = 128 bits (319), Expect = 2e-29  
Identities = 58/92 (63%), Positives = 65/92 (70%)

Query: 35 CNVEMLPAPAPNLTDDEPPIGYIANTBCRPGYSGRPSIICLNKSWTSADCKCR 94  
C P +FA+ T+ +PPIGT L YECRP Y GRPSI CL N VM+S KD CKR  
Query: 452 CQAPDHFLPAKLTQYNASDPPIGTSLKRYCRPEYGRPFSITCLDNLMWSSPDVVC 511  
CQAPDHFLPAKLTQYNASDPPIGTSLKRYCRPEYGRPFSITCLDNLMWSSPDVVC  
Query: 95 KSCNPPDPVNGMAHVIKDIQSGQIKYSCPG 126  
SC+ PDPVNGMAHV IKDIQSG+I YSC G  
Query: 512 KSCNPPDPVNGMAHVIKDIQSGQIKYSCPG 543  
KSCNPPDPVNGMAHV IKDIQSGQIKYSC PG

Score = 68.7 bits (165), Expect = 3e-11  
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSFSQCNVEMLPAPAPNLTDDEPPIGYIANTBCRPGYSGRPSIICLNKSWTSADCKCR 86  
L S S C P + A T D P G + Y C PGY R S+ C W+  
Query: 249 LPSQCNVEMLPAPAPNLTDDEPPIGYIANTBCRPGYSGRPSIICLNKSWTSADCKCR 307  
LPSQCNVEMLPAPAPNLTDDEPPIGYIANTBCRPGYSGRPSIICLNKSWTSADCKCR  
Query: 87 AKXCKRSCRN-PDPVNGMAHVIKDIQSGQIKYSCPGYRLIGSSSANCIIISGNVIMDKTPVC 145  
AKXCKRSCRN-PDPVNGMAHV IKDIQSGQIKYSC PGYRLIGSSSANCIIISGNVIMDKTPVC  
Query: 308 AATPCVSCDQDQGLNGVLPVNLQAKAVDVCDFOLKSSASTCVLAWESL 367  
AATPCVSCDQDQGLNGVLPVNLQAKAVDVCDFOLKSSASTCVLAWESL  
Query: 146 WDKTPVC 154  
W+ + VC+  
Query: 368 WNSVPC 376  
W+ + VC+

Score = 44.1 bits (102), Expect = 7e-04  
Identities = 30/113 (26%), Positives = 45/113 (39%), Gaps = 13/113 (11%)  
Query: 54 EPIGYIANTBCRPGYSGRPSIICLNKSWTSADCKCRSCNPPDPVNGMAHVIMDKTPVC 107  
+G + Y C GY S II +W + C R C PP NG ++  
Query: 79 DIQSGQIKYSCPGYRLIGSSSANCIIISGNVIMDKTPVCIRICGLPPTITMDNIS 138  
DIQSGQIKYSCPGYRLIGSSSANCIIISGNVIMDKTPVCIRICGLPPTITMDNIS

Query: 108 HWIKDIQSGQIKYSCPGYSGRPSIICLNKSWTSADCKCR 153  
++ +G S C G +L+G S C + + V IM P C  
Query: 139 TURENFHYGVSIVYACNPGSGGRKVFELVGRPSIYCTSDQVIGWSPAPFC 191  
TURENFHYGVSIVYACNPGSGGRKVFELVGRPSIYCTSDQVIGWSPAPFC

Score = 41.4 bits (95), Expect = 0.005  
Identities = 30/112 (26%), Positives = 50/112 (44%), Gaps = 17/112 (15%)

Query: 57 IGYIANTBCRPGYSGRPSIICLNKSWTSADCKCRSCNPPDPVNGMAHVIMDKTPVC 112  
+G +++ C G+ S ++ S+W S+ C++ NG R  
Query: 337 LQAKVDCDEBQGLKSSASVYLAGESLWNSVPCQIPCSPPVYIENG-RHNGK 395  
LQAKVDCDEBQGLKSSASVYLAGESLWNSVPCQIPCSPPVYIENG-RHNGK  
Query: 113 IQ--FGSQIKYSCPGYRLIGSSSANCIIISGNVIMDKTPVC 153  
IQ--FGSQIKYSCPGYRLIGSSSANCIIISGNVIMDKTPVC  
Query: 396 LQVWSPAPRGILGHCOAHPDLFAKLQYNASDPPIGTSLKRYCRPEY-YGRPFSITCL- 496  
LQVWSPAPRGILGHCOAHPDLFAKLQYNASDPPIGTSLKRYCRPEY-YGRPFSITCL-

Score = 34.0 bits (76), Expect = 0.76  
Identities = 32/138 (23%), Positives = 50/138 (36%), Gaps = 29/138 (21%)

Query: 37 VEMLPAPAPNLTDDEPPIGYIANTBCRPGYSGRPSIICLNKSWTSADCKCR 81  
+P LP PT DF F G+ + Y C EG GR SI C N  
Query: 123 ICGLP---PITNGDPITNRENFHYGVSIVYACNPGSGGRKVFELVGRPSIYCTSDND 179  
ICGLP---PITNGDPITNRENFHYGVSIVYACNPGSGGRKVFELVGRPSIYCTSDND  
Query: 82 --SWTSADCKCRSCNPPDPVNGMAHVIMDKTPVC---IQFGSQIKYSCPGYRLIGSSS 135  
--SWTSADCKCRSCNPPDPVNGMAHVIMDKTPVC---IQFGSQIKYSCPGYRLIGSSS  
Query: 180 QVIGWSPAPRGILGHCOAHPDLFAKLQYNASDPPIGTSLKRYCRPEY-YGRPFSITCL- 237  
QVIGWSPAPRGILGHCOAHPDLFAKLQYNASDPPIGTSLKRYCRPEY-YGRPFSITCL-  
Query: 136 KQALNK---WEPDFSC 252  
KQALNK---WEPDFSC

Score = 32.8 bits (73), Expect = 1.7  
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)

Query: 35 CNVEMLPAPAPNLTDDEPPIGYIANTBCRPGYSGRPSIICLNKSWTSADCKCR 83  
C P +P R T + P P G +NY C P G F +I C N V  
Query: 380 CSPSPVITNGHHTGKPLEY-FPPGKAVNYTDDPHDRGTSFDLIGESTIRCTSDPQNGV 438  
CSPSPVITNGHHTGKPLEY-FPPGKAVNYTDDPHDRGTSFDLIGESTIRCTSDPQNGV  
Query: 84 WTSADCKR-RKSCNPPDPVNGMAHV---IKDIQSGQIKYSCPGYRLIGSSSANCII 139  
WTSADCKR-RKSCNPPDPVNGMAHV---IKDIQSGQIKYSCPGYRLIGSSSANCII  
Query: 439 WSSPAPRGILGHCOAHPDLFAKLQYNASDPPIGTSLKRYCRPEY-YGRPFSITCL- 496  
WSSPAPRGILGHCOAHPDLFAKLQYNASDPPIGTSLKRYCRPEY-YGRPFSITCL-  
Query: 140 SGNVYIMDKTPVC 153  
SGNVYIMDKTPVC  
Query: 497 --DNLMWSSPDVVC 508  
DNLMWSSPDVVC

>GSEQ:AA28552 Membrane targeted complement inhibitor peptide.

Length = 198

Score = 251 bits (635), Expect = 2e-66  
Identities = 110/121 (90%), Positives = 116/121 (94%)

Query: 34 QCNVEMLPAPAPNLTDDEPPIGYIANTBCRPGYSGRPSIICLNKSWTSADCKCR 93  
QCN PEARPPNLTD+PEPPIGYIANTBCRPGYSGRPSIICLNKSWT AKD+C+R  
Query: 2 QCNAPMLPAPAPNLTDDEPPIGYIANTBCRPGYSGRPSIICLNKSWTADCKCR 61  
QCNAPMLPAPAPNLTDDEPPIGYIANTBCRPGYSGRPSIICLNKSWTADCKCR  
Query: 94 KSCNPPDPVNGMAHVIKDIQSGQIKYSCPGYRLIGSSSANCIIISGNVIMDKTPVC 153  
KSCNPPDPVNGMAHV IKDIQSGQIKYSC PGYRLIGSSSANCIIISGNVIMDKTPVC  
Query: 62 KSCNPPDPVNGMAHVIKDIQSGQIKYSCPGYRLIGSSSANCIIISGNVIMDKTPVC 121  
KSCNPPDPVNGMAHV IKDIQSGQIKYSC PGYRLIGSSSANCIIISGNVIMDKTPVC  
Query: 154 D 154  
D

D  
Sbjct: 122 D 122

Score = 43.8 bits (101), Expect = 9e-04  
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GYTLNTECRPGY---SGRPSITICLNKSVWSAKDKCKRSCRPDPVNG--MAHYIA 111  
G+ + Y C GR S II \*W+ C R C R P NG ++ +  
Sbjct: 84 GSQIKYSCGTGRLLIGSSATCIIISGDTVMDEPFCIDRIPGLPTINMGFISTNRE 143  
Query: 112 DIQFGSQIKYSCPKG-----YRLIGSSATCIIISGNTV-INDNKTPTVC 153  
+ +GS + Y C G + L+G S C + + V IW P C  
Sbjct: 144 NFHYGSVVTYRCNPGSGRKVFELVGEPSITCTSNDDQVIGNSGAPQC 192

>GSEQ:AA26817 Membrane targeted complement inhibitor peptide.  
Length = 198

Score = 251 bits (635), Expect = 2e-66  
Identities = 110/121 (90%), Positives = 116/121 (94%)

Query: 34 OCNVPEMLPPAPPTNLDDEPPIGTLYNTECRPGYSGRPSITICLNKSVWSAKDKCKR 93  
OCN PEMLPPAPPTNLD+PEPPIGTLYNTECRPGYSGRPSITICLNKSVWT AED+C+R  
Sbjct: 2 OCNAPEMLPPAPPTNLDDEPPIGTLYNTECRPGYSGRPSITICLNKSVWSAKDKCKR 61  
Query: 94 KSCRNPPDPVNGMAHYIKEDIQFGSQIKYSCPKGRLLIGSSATCIIISGNTVINDNKTPTVC 153  
KSCRNPPDPVNGR HVIK IQFGSQIKYSC KGRLLIGSSATCIIISG+IVINDN+TF+C  
Sbjct: 62 KSCRNPPDPVNGMAHYIKIQFGSQIKYSCGTGRLLIGSSATCIIISGDTVMDEPFC 121  
Query: 154 D 154  
Sbjct: 122 D 122

Score = 43.8 bits (101), Expect = 9e-04  
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GYTLNTECRPGY---SGRPSITICLNKSVWSAKDKCKRSCRPDPVNG--MAHYIA 111  
G+ + Y C GR S II \*W+ C R C R P NG ++ +  
Sbjct: 84 GSQIKYSCGTGRLLIGSSATCIIISGDTVMDEPFCIDRIPGLPTINMGFISTNRE 143  
Query: 112 DIQFGSQIKYSCPKG-----YRLIGSSATCIIISGNTV-INDNKTPTVC 153  
+ +GS + Y C G + L+G S C + + V IW P C  
Sbjct: 144 NFHYGSVVTYRCNPGSGRKVFELVGEPSITCTSNDDQVIGNSGAPQC 192

Database: Current.Geneseq.AA.fasta  
Posted date: Apr 14, 2003 12:19 PM  
Number of letters in database: 150,621,602  
Number of sequences in database: 1,029,157

Lambda K H  
0.323 0.140 0.456

Gapped Lambda K H  
0.270 0.0470 0.230

Matrix: BLOSUM62  
Gap penalties: Existence: 11, Extension: 1  
Number of hits to DB: 62/90668  
Number of Sequences: 1029157  
Number of extensions: 2617728

Number of successful extensions: 10088  
Number of sequences better than 10.0: 685  
Number of HSP's better than 10.0 without gapping: 286  
Number of HSP's successfully gapped in prelim test: 399  
Number of HSP's that attempted gapping in prelim test: 6318  
Number of HSP's gapped (non-prelim): 2814  
length of query: 174  
length of database: 150,621,602  
effective HSP length: 46  
effective length of query: 128  
effective length of database: 103,280,380  
effective search space: 1321988640  
effective search space used: 1321988640  
T: 11  
A: 40  
X1: 16 ( 7.5 bits)  
X2: 38 (14.8 bits)  
X3: 64 (24.9 bits)  
S1: 41 (21.9 bits)

### Graphical Viewer...

Submit sequences to: BLAST2







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CLUSTAL W (1.7) Multiple Sequence Alignments

$$\frac{325}{627} \times 100\% = 51.8\%$$

```
Aligning...
Sequences (1:2) Aligned, Score: 60
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences: 2      Score: 8429
Alignment Score 3045
CLUSTALW-Alignment file created [ba0NMay0L.atn]
CLUSTAL W (1.7) multiple sequence alignment
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103561CBI	CGGACTCAGAGGGAATGCCCTGAGTGGCTTGGCTTTGGTTGGCTTCCAGACCTTCCGGAAT
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GSBO_AA238150	GAATGGGGGCTCTTCTCCAGAGAGCCCGAGCTGTGGC--CGCGGCGC-CCGGTTC
103561CBI	AAATACGGGGATCCCGCGCGCTCATGAGAGCTCCCGCTCGTCTGATGAGAGTCCCTTT
	***** * * * *
GSBO_AA238150	TCCTCTTTCAGTCCGAGAGGATCCCTGCTGGCGGTGTGGTGCCTCTTCCGCTCCCGAGTGG
103561CBI	CTTCCGCGGCTTCTCGGGTGGTCTTTCGCGCGCTCGAGTGTACT--GCTGTCCTCT
	*** *****
GSBO_AA238150	CTTGGGGTCAATGCAATGCCCCAGAAATGGCTTCTCATTTGCTCCAGGCGCAACCAACTAATG
103561CBI	TCTTCAGTAAATGCAATGTCGCGGAAATGGCTTTCAGTATTCACAGGCGCCCAACCACTAATG
	** *****
GSBO_AA238150	ATGAGTTTAAAGTTTCCCATTTGGGACAATCTTGAACTATGATGCCCGCTGGTTATTCG
103561CBI	ATGACTTTAAGTTTCCCATTTGGGACAATCTTAACTATGAAATGCGCGCTGATTTATTCG
	*****
GSBO_AA238150	GAAGCCGTTTTCTATCATCTGACCTTAAAAAACTCAAGTCTGACATGCTGCTAAAGGACAGGT
103561CBI	GAAGCCGTTTTCTATCATCTGACCTTAAAAAACTCAAGTCTGAGCAAGTGTGCTAAAGGACAAAT

5/5/03 9:06 PM

[illegible]

ClusterW Results		http://patents.incyte.com:8000/cgi-bin/SqSServer/SqSServer	ClusterW Results	http://patents.incyte.com:8000/cgi-bin/SqSServer/SqSServer
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GSBQ_AA238150 103561CB1	GAAGTCTTCCCTTTTGGAAAAAGAGTAAATTACATGCGAAGCCCCACCCAGACAGAGGG	GSBQ_AA238150 103561CB1	CGTACCCCAAGGACAAAGGACAACTTTTCAACCCGGGACAGGAAGTGTCTCAAGCTGTAG	
GSBQ_AA238150 103561CB1	ACGAGCTTCGACCTCATTTGGAGAGAGACACATCCGCTGCAAAATGTGACCTTCAAAGGAAAT	GSBQ_AA238150 103561CB1	CCCGGCTAATGACCTTCAGAGGGGGTCCGCTAATGCGTGCACACCCCAAGGAGACTGGAGC	
GSBQ_AA238150 103561CB1	GGGGTTTGGAGACGCCCTGCCCCCTCGCTGTGGAAATTCGTGGTCACTGTCAAGCCCCAGAT	GSBQ_AA238150 103561CB1	CTTCGACGCCCCCAATGTGAATGTGAATTCCTGTGATGACCTTCATGGGCCAACTTCCTTAAT	
GSBQ_AA238150 103561CB1	CAATTTCTGTGTTGGCAATGGTGA AAAACCAAAACCAATGCAATGCACTTTCCATTGGGACA	GSBQ_AA238150 103561CB1	GGCCGTGTGCTATTTTCCAGTAAATCTCCAGCTTGGAGCAAAAGTGGATTTTGTGTGTGAT	
GSBQ_AA238150 103561CB1	TCCTTAAAGTACGAATGCCGTCCTGAGTACTAGGGAGGCCATTCCTCTATCAATGTCTA	GSBQ_AA238150 103561CB1	GAAAGATTTCAATTTAAAAGGCAAGCTCTGCTAATGTATGTGTCTTGGCTGGAAATGGAAAGC	
GSBQ_AA238150 103561CB1	GATTAACCTGTGCTGTGTCAAAGTCCCAAAAGATGCTGTAAACGTAAATCATGTAAACCTCCT	GSBQ_AA238150 103561CB1	CTTTGGAAATAGCAGTGTTCAGATGTGTGGAACAAATCTTTTGTTCAAAGTCTCCAGTTAAT	
GSBQ_AA238150 103561CB1	CCAGATTCAGTGAATGGCAGTGTGTGCAATGTGATCAAGAGATCCAGTGTGGATCCAGAAATC	GSBQ_AA238150 103561CB1	CCTAATGGGAGACACACAGGAAAACTCTGGAAGTCTTTCCTTTGGAAAAAGCAGTAAAT	
GSBQ_AA238150 103561CB1	AACTATCTGTGTACTACAGGGACCGACTCATTTGTGTACTCATCTGTGATGTATCTCTC	GSBQ_AA238150 103561CB1	TACACATGCGACCCCTCACCCAGACAGAGGAGCAGAGCTTCGACTCTCATTTGGAGAGACACC	
GSBQ_AA238150 103561CB1	TCGGGCAATGCTGCCCAATGGAGCAGAGGCCGCCAATTTGTCTAAACGAATTCCTGTGGG	GSBQ_AA238150 103561CB1	ATCCGCTGCACAATGTAACCTCTAAGGGAATGGGGTTTGGAGCAGCCCTGCCCCCTGCTGT	
GSBQ_AA238150 103561CB1	CTAACCCCCACCATGCGCAATGAGATTTTCTATTAACACACAGAGAGAAATTTTCTACTAT	GSBQ_AA238150 103561CB1	GGAAATCTGTGGGTCACTGTCAAGCCCAAGATCAATTTTCTGTGTTGCCAATGGTGA AAAACCA	
GSBQ_AA238150 103561CB1	GGATCAGTGTGTACTTACCGCTGCAATCTCTGGAAGCGAGGAGGA AAAAGTGTGTGAGCTT	GSBQ_AA238150 103561CB1	ACCAATGCATGTGACTTTCCATTGGGACATCTTTTAAAGTACGAATGCCGTCTGTAAC	
GSBQ_AA238150 103561CB1	GTGGGTGAGGCCCTCCATATATGCAACGACAAATGACGAATGAGTGAATGTGGGCAATCGAGCGC	GSBQ_AA238150 103561CB1	TACGGGAGGCCATTCCTATATCATATGTCTAGATTAACTGTGTGTGTGTCAAAGTCCCAAGAT	
GSBQ_AA238150 103561CB1	CCGGCCCCCTCATGTGCAATTAATCTTAACAAATGCAACGCTCCAAATGTGGAAAAATGGAATA	GSBQ_AA238150 103561CB1	GTCTGTAAACGTAAATCAATGTAAATCTCTCCAGATTCACATGGAATGGCAATGGTGCATGTG	
GSBQ_AA238150 103561CB1	TTGGTATCTGCAACAGAGCTTATTTTCTTAAATGAATGTGTGGAATTTAGTGTGTGACG	GSBQ_AA238150 103561CB1	ATTCACAGACATTCAGGTTGGATTCAGAAATCAATCTATTTCTGTGTACTACAGGGCACCGACTC	
GSBQ_AA238150 103561CB1	CTGTGCTTTGTCAATGAAGAACCCCGCCTGTGAAATGTGCAGGCCCTGAAACAAATGGAGAG	GSBQ_AA238150 103561CB1	ATTGGTCACTCATCTGTGAAATGTATTCCTCTCAGGCAATACCTGCCCATTTGAGACAGAAAG	
		GSBQ_AA238150	CCGGCCAAATTTGTCAACGAATTCCTTGTGGGCTTACCCCAACCATGTGCCAATGGAGATTTTC	



GSBQ\_AA238150  
103561CB1  
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-----  
GTTTCGANTGAAGGTTCCGATTAAAGCAGAGTCTGTACTCATTTGTCTCTGGCTGCA  
-----  
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GSBQ\_AA238150  
103561CB1  
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-----  
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-----  
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-----  
GSBQ\_AA238150  
103561CB1  
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-----  
CATTCATTTGAGAGAACGTATCTCTAATATCTTCCTGGAGTGAATACAGCTACATTTGT  
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GACCCCGGCTACCTGTATGTGGAAAGGGCTTCAATTTCTGTACAGACAGGGAATGTGG  
-----  
AACCATTGTGATCATTTATTTGCAAGAAATTTGTATGCTTCCCATGTTTATGAAATGCA  
-----  
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TGTGAAGATGGGTATACCTCTGGAAGGCAGTCCCTGGAGGCAAGTCCAGGCGGATGACAGA  
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TGGGACCTCTCTCTGGCCAAATGTACCTCTCTGTGACATGATGCTCTCATAGTTGACACT  
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103561CB1

GSBQ\_AA238150  
103561CB1  
CTTCCTTGAACAAGTACTATAGAGCTGTAAGAACATCTCTGAATATCAATTTTGTGTGGGAAAG  
-----  
GAGCCAAATGATTTTCAACAGAAATCAGATCTGAGCTTCAATTAAGTCTTTGAAGTGAATCTCA  
-----  
GAGAGACGACACATGTGCACTTGAAGAATGCTGCCCCCTTCCCTGTGATCTTACGAAAGCTC  
-----  
CTGCCCTCTTGTGTGTCACCTGTGAAACCCCAACCTTCTGCTGCTGTGCTTAAACGACACA  
-----  
CAGTATCTATGTCAGGGGAAAAACATGCAATTTAGAGAGATAGAAATATGTTTGTGATTTACTTA  
-----  
AAGGAATTAAGGTGTGCTGTGGAATTTCTGTGTTTGAAGTGTGACATGTCTTTTTTAAA  
-----  
ATATTTGTATTAATGGAATGGGCTCAGTAAAGAGACCTTGAATAATGCAAGAAATGTAATGA  
-----  
AAATATGTCACCTTAATATATGCTATCTTACTGATTAACACATCTCTAATATTTTGAATTCATT  
-----  
TTCTGCTTATCTTCTTTCACATATGTGTTTTTATCATAGTACTTTTCCCCCTTAAGTT  
-----  
TGTTCCTTTTATTTTATTAAGAGAAACCTTATGCTTTTAAACAGTTTAAAGTGAATAT  
-----  
ATGCTATATCAAGTTTTTATCTTCTCTAGGAGAAAAATTAATTTTACTTGAAGAACGATGA  
-----  
ATGATCATGGGAAGAGTGTAAAGTACTGAAGAAATATTTGGAATAATTAAGATTTCTG  
-----  
AATTCCTCTTTTTTTTGAATGAGATGATGCTGTGCTGTCTCCAGGCTGGAAGTCAAGTGC  
-----  
GTAATCTGAGCTCACTGCAACGTCCGCTCCCG  
-----  
GSBQ\_AA238150  
103561CB1

Submit sequences to: BLAST2



ID	AA38150	14867ac5163e7e04c7b1d831b469abbl
CS	AA38150	standard; DNA, 6951 BP.
IDH	DNA	
MO	DNA	
DV	20-MAR-2003 (updated)	
DT1	22-FEB-2000 (first entry)	
DT2	22-FEB-2000	
DT	PATENT US5981481-A	
AK	PRIMARY AC	AA38150
EAK		
DR	P-PSDB	AAV55751
EDR	WPI	1999-633357/54
D8	Human C3b/C4b receptor (CRI) protein encoding DNA.	
KW	Arthus reaction	
KW	C3b/C4b receptor	
KW	CRI protein	
KW	autoimmune disorder	
KW	cell-surface protein	
KW	complement pathway enzyme	
KW	complement regulatory activity	
KW	diagnostic	
KW	erythrocyte	
KW	heart condition	
KW	human	
KW	inflammation	
KW	myocardial infarct	
KW	reperfusion injury	
KW	ss	
KW	tissue damage	
KW		
OS	Homo sapiens.	
SC	4a22b9c1dbf65eca55a08e9eb4312aee	
SP	HOMO SAPIENS	
E5P		
INST	(AAVAN) AVANT IMMUNOTHERAPEUTICS INC	
CC	The invention relates to a human C3b/C4b receptor (CRI) protein. The CRI	
CC	protein or fragment is expressed as a cell-surface protein on the surface	
CC	of a non-human cell and exhibits a complement regulatory activity of full	
CC	-length human CRI as expressed on erythrocytes. The CRI function in vivo	
CC	may be mediated through the inhibition of complement pathway enzymes. The	
CC	soluble CRI protein exhibits a complement regulatory activity, and this	
CC	may be used to prevent reperfusion injury, inhibit Arthus reaction, and	
CC	neutrophil mediated tissue damage, and reduce myocardial infarct size,	
CC	and inflammation. The CRI protein and its fragments can also be used in	
CC	the treatment of conditions which involve unwanted complement activity,	
CC	e.g. shock lung, tissue damage due to burn, or ischemic heart conditions,	
CC	and autoimmune disorders. CRI proteins, analogues, derivatives, and anti	
CC	-CRI antibodies are used in assays, and diagnostics. The present sequence	
CC	represents a DNA encoding the human CRI protein.	
CC	(Updated on 20-MAR-2003 to correct PR field.)	
ECC		
RN	1	fe0184ae97550b668750b1a74d037fed
RC	PD: 09-NOV-1999. PF: 06-JUN-1995; 95US-0470652. PR: 03-APR-1989; 89US-0332865.	
RT	24-FEB-1993; 93US-0026134. PR: 06-DEC-1994; 94US-0350238. PR: 01-APR-1988; 88U	
RL	A human C3b/C4b receptor (CRI) protein having antiinflammatory and cardiant ac	
RA	Patent: US5981481-A. Disclosure; Fig 1A-P; 87dp; English.	
RA	Concino M. F.	CONCINO MF
RA	Mong W. W.	WONG WW
RA	Makrides S. C.	MAKRIDES SC
RA	Klickstein L. B.	RICKSTEIN LB
RA	Peaton D. T.	PEATON DT
RA	Ip S. H.	IP SH
RA	Marsh H. C.	MARSH HC

[illegible]

ESQ

### BLAST2 Search Results

NCBI-BLASTN 2.0.10 [Aug-26-1999]

Query= 103561CBI  
(627 letters)

Database: Current.Geneseq.NA.fasta.  
2,461,325 sequences; 1,289,285,926 total letters

```
Searching.....done
```

### Sequences producing significant alignments:

Sequences producing significant alignments:	Score (bits)	E Value
✓ GSEQ:AAFS602 Human RECAP polynucleotide, SEQ ID NO: 30.	1243	0.0
✓ GSEQ:ABQ9306 Human coding sequence SEQ ID 39.	1229	0.0
✓ GSEQ:AAS6422 DNA encoding novel human diagnostic protein #94	682	0.0
✓ GSEQ:ABX34686 Human mdtc cDNA SEQ ID 247.	599	e-169
✓ GSEQ:ABA91636 Human C3b/C4b receptor CR1 (complement receptor	599	e-169
✓ GSEQ:AKR84738 Human cDNA differentially expressed in granuloc	599	e-169
✓ GSEQ:AAI58380 Human polynucleotide SEQ ID NO 583.	599	e-169
✓ GSEQ:AAZ381650 Human C3b/C4b receptor (CR1) protein encoding D	599	e-169
✓ GSEQ:AAQ11642 Entire human complement type 1 receptor coding	599	e-169
✓ GSEQ:AAW91477 CR1 protein DNA.	599	e-169

>GSEQ:AAF58602 Human RECAP polynucleotide, SEQ ID NO: 30

**Length = 627**

Score = 1243 bits (627), Expect = 0.0  
Identities = 627/627 (100%)

Strand = Plus / Plus

### BLAST2 Results

```
Query: 1 cggactcagaagvggacttccccctgcctcgcccttcgtttcttcctgccacctccggat 60  
          |||||  
Sbjct: 1 cggactcagaagvggacttccccctgcctcgcccttcgtttcttcctgccacctccggat 60
```

```
Query: 61 aaatcacgggggtctcccgccgcgcctcatgagcgctccgctcgcgtctcgagcgctcccttc 120
          |||||
Sbjct: 61 aaatcacgggggtctcccgccgcgcctcatgagcgctcccgctcgcgtctcgagcgctcccttc 120
```

**Query:** 121 cttcccgagcttcttcgtgattgcctcctggcgccttgctgtcgtcgtccccctct 180  
**Sbjct:** 121 ctcccgagcgtctctcctggtgtgccttcctggccccttgctgtcgtcgtccccctct 180

**Query:** 181 ccgattcaatgcgaatgtcccggaatccttcccatttcggcagcctaccacctaacttgatg 240  
|||||  
**Sbjct:** 181 ccgatcatgcgaatgtcccggaatccttccatttcggcaggctataccaactaatgatg 240

Query: 241 accttgaagttccccaatgtggacatactgaactaagaatcgccctgtttatccggaa 300  
|||||  
Sbjct: 241 accttgaagttccccaatgtggacatactgaactaagaatcgccctgtttatccggaa 300

**Query:** 301 gaccggttttcatacatctgcgttaaaaaaacccagttcttgacaaagtgtcctaagrgaaccaagtga 360  
**Sbjct:** 301 gaccggttttcatacatctgcgttaaaaaaacccagttcttgacaaagtgtcctaagrgaaccaagtga 360

Query: 361 aacgttaatacatgctgtaatccctccagatccctgtgatatgcatgycacacatgtatcaaaag 422  
|||||  
Sbjct: 361 aacgttaatacatgctgtaatccctccagatccctgtgatatgcatgycacacatgtatcaaaag 422

```

Query: 421 acatccagttcgcgatcccaataataatctctgtccctaaaggataccgcattggtc 488
          |||
Sbjct: 421 acatccagttcgcgatcccaataataatctctgtccctaaaggataccgcattggtc 488

```

```
Query: 481 cctcgtctgcacatgcatacctcaggaacacactgtcatttggtaataaacccttg 54
          |||||
Sbjct: 481 cctcgtctgcacatgcatacctcaggaacacactgtcatttggtaataaacccttg 54
```

```
Query: 541 ttctgtagcagtcgagttctaaatgcattcccttctttaccggaatacttcaatttc 60
          |||||
Sbjct: 541 ttctgtagcagtcgagttctgaatatgcattcccttctttaccggaatacttcaatttc 60
```

```

Query: 601 ctctcggaataataaaaatcctaaccga 627
      |||||
Sbjct: 601 ctctcggaataataaaaatcctaaccga 627

```

>GSEQ:ABQ99306 Human coding sequence SEQ ID 39

**Length = 677**

Score = 1229 bits (620), Expect = 0.0

Strand = Plus / Plus

Query: 1 cggaactcagaaaggacttccctcgtcgtgcgttcctcgtttctctcgtcaccctccgat 60

Sbjct: 39  
cgagactcgaagugactccctcgtccgcgtcgtccttcggtctctctgctacactccgat 98

```

Query: 61 aaatcacgggggtctcccgccgctcatggcgagctccgctcagcgtcttc 120
          |||||
Sbjct: 99 aaatcacgggggtctcccgccgctcatggcgagctccgctcagcgtcttc 158

```

```
Query: 121 cttcccgagcgtcttctcttgagtctcttcgacggccctctgtctgcctctctt 180
|||||
|||
Sbjct: 159 ctcccgcgcgtcttctcttgagtctcttcgacggccctctgtctgcctctctt 218
```

```
Query: 181 ccgacccaatgccaatgtcccggaatgcttcattgccaagccccaactaactgatg 240
          |||||
Sbjct: 219 ccgacccaatgccaatgtcccggaatgcttcattgccaagccccaactaactgatg 278
```

Query: 241 actcttgaggtctcccatgtggacatactgaactatgaatgcgcgcctggttatccgaa 300  
 |||||  
 Sbjc: 279 actcttgaggtctcccatgtggacatactgaactatgaatgcgcgcctggttatccgaa 338

Query: 301 gacccgtttcttcatacatctgcctaaaaaactcagtcctgcacaagtgtctaagagacaagtgc 360  
 |||||  
 Sbjct: 339 gaccgtttcttcatacatcctgcctaaaaaactcagtcctgcacaagtgtctaagagacaagtgc 398

Query: 361 aacgtaaatcatctgttcgtaatccctccagatctctgtaatgycatgycacatgtgtatcaag 420  
 |||||  
 Sbjct: 399 aacgtaaatcatctgttcgtaatccctccagatctctgtaatgycatgycacatgtgtatcaag 458

Query: 421 acatccagttcgcgaatccaataataatctctgtcccaagataccgaactatggt 480  
 |||||  
 Sbjct: 459 acatccagttcgcgaatccaataataatctctgtcccaagataccgaactatggt 518

Query: 481 cccgcgtctgccacatgcatcatctcaggcaaacctgtcatctggagataaaacacctg 540  
|||||  
Sbjct: 519 ccccgtctgccacatgcatcatctcaggcaaacctgtcatctggagataaaacacctg 578

Query: 541 ttctgtgacagtgagtgaatatgcattccatttccttaccgatcacatctcaattttc 600  
|||||  
|||  
Subject: 579 ttctgtgacagtgagtgaatatgcattccatttccttaccgatcacatctcaatttt 638

```

Query: 601 ctctggaataataaaatct 620
          |||||
Sbjct: 639 ctctggaataataaaatct 658

```

>GSEQ:AAS64290 DNA encoding novel human diagnostic protein #94.  
Length = 9038

Score = 682 bits (344), Expect = 0.0  
Identities = 546/580 (94%), Gaps = 30/580 (5%)  
Strand = Plus / Plus

Query: 1  
cggaactcagaagggactccctcgtcgtgactgcatttcggttctctctgcacaccctcgat 60  
|||||  
Sbjct: 1583  
cggaactcagaagggactccctcgtcgtgactgcatttcggttctctctgcacaccctcgat 1622

Query: 61  
aaatcacggggtctctcccgcgccgctcatggcgccctcccgctcgtctctcgagcgtccc-ttt 119

**Sbjct: 1643 aatcacgggtctccgcgcgcgtcatggcgctcccgctcctcgcgagcgctccctt 1702**

Query: 120 ccttcccgcgcttctct-gggtctgctctgagcgccct-gtgttgcctgcctgtcctcct 177

Sbjct: 1703 cctcccgcgcttctcctgggtctgcttctcggcgccctgggtgtgcttgcctgcctgcctcct 1762

Query: 178 tctccgaatcaat-gcaatatgcccgaaat-aacctcca-tttgcca--gagctgac-accac 331

Sbjct: 1763 tctccgatcatgcatgtcccggaatggtcttcatttgcacagggtcttaccaaacc 1822

**QUESTION**

Subject: 1823

343

Query: 344  
tcgctaaggacaaagtgcacaaag-tcaatcatg-tcgtaatcc-tccagatcctgtgaat-g 399

Accession: AF021532

Query: 400 gcatggcacatgt--atcaagacatccag-ttcgga-tcccaa-ttaatatcttg 454

Sbjct: 2003 gcatggcacatgtgatccaagacatccagtttcgattcccaatttaatatcttg 206;

[illegible]

Subjct: 2063 ttctaagatataccgactcatgtggttcctcgtctgccaatgqcatcatctcaagca 2122

3  
2  
1  
:  
21  
22  
23

Score = 97.0 Dots (45), Expect = 3e-18  
Identities = 130/157 (82%)

Query: 360  
aaacgttaatcatgtcgttaatccctccagatccctgtgaatggcatggcacatgtgatcaa 419

SpJct: 46/2 aaacgtaatcatgtataaacctcctccagatccagtgatgcatgtgcatacaca 4731

Query: 420 gacatccagttcggatccccaattaaatatcttqtctctaaagqataaccgaatcattat 479

Sbjct: 4732 gacatccaggttgatccagaatcaactatctctgtactacagggcaccgactcatgtg 4791

**Amount:** 480  
+-----+

Subject: 4792 cactcactcttcaatnatacccttcacccccaaatactt 1028



Score = 95.6 bits (48), Expect = 1e-17  
Identities = 102/120 (85%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcgtcgttaatccctccagatccctggaatgcatgagcatgcatcaaa 419  
|||||  
Sbjct: 3322 aaacgtaaatcgtcgttaatccctccagatccctggaatgcatgagcatgcatca 3381

Query: 420 gacatccagttcggatcccaaatatattctgtcctaaggataccgactcattggt 479  
|||||  
Sbjct: 3382 gacatccagttcggatcccaaatatattctgtcctaaggataccgactcattggt 3441

Score = 61.9 bits (31), Expect = 2e-07  
Identities = 73/87 (83%)  
Strand = Plus / Plus

Query: 208 ttccatttgcaggccctaccacctaactgagtttgaatttcccatgaggacatc 267  
|||||  
Sbjct: 5879 ttccatttgcaggccctaccacctaactgagtttgaatttcccatgaggacatc 5938

Query: 268 tgaactatgaaatgacgcgcctggttatt 294  
|||||  
Sbjct: 5939 tgaactatgaaatgacgcgcctggttatt 5965

>GSEBQ.ABX34686 Human mdm2 cDNA SEQ ID 247.  
Length = 7385

Score = 599 bits (302), Expect = e-169  
Identities = 350/366 (95%)  
Strand = Plus / Plus

Query: 185 tcaatgcaatgctccggaatggtcttccatttgcaggccctaccacctaactgagatt 244  
|||||  
Sbjct: 153 tcaatgcaatgctccggaatggtcttccatttgcaggccctaccacctaactgagatt 212

Query: 245 tgaatttcccatctgggacatactgaaactatgaaatgacgcgcctggttattccggaagacc 304  
|||||  
Sbjct: 213 tgaatttcccatctgggacatactgaaactatgaaatgacgcgcctggttattccggaagacc 272

Query: 305 gttttctatcatctgtcctaaataaactcagcttggacaagtgtgtaaggacaagtgcgaagc 364  
|||||  
Sbjct: 273 gttttctatcatctgtcctaaataaactcagcttggacaagtgtgtaaggacaagtgcgaagc 332

Query: 365 taaatcatgctgaatcctccagatcctgtgaaatgcatgagacatgcatcaagaagat 424  
|||||  
Sbjct: 333 taaatcatgctgaatcctccagatcctgtgaaatgcatgagacatgcatcaagaagat 392

Query: 425 ccagttcggatcccaaatatattctgtcctaaggataccgactcattggtcttc 484  
|||||  
Sbjct: 393 ccagttcggatcccaaatatattctgtcctaaggataccgactcattggtcttc 452

Query: 485 gtcctgcacatgcatcattccaggcaaacatgcatcttggatataaacaacctgtttg 544  
|||||  
Sbjct: 453 gtcctgcacatgcatcattccaggcaaacatgcatcattggatataaacaacctgtttg 512

Query: 545 tgacag 550  
|||||  
Sbjct: 513 tgacag 518

Score = 97.6 bits (49), Expect = 3e-18  
Identities = 130/157 (82%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcgtcgttaatccctccagatccctggaatgcatgagcatgcatcaaa 419  
|||||  
Sbjct: 3028 aaacgtaaatcgtcgttaatccctccagatccctggaatgcatgagcatgcatcaaa 3087

Query: 420 gacatccagttcggatcccaaatatattctgtcctaaggataccgactcattggt 479  
|||||  
Sbjct: 3088 gacatccagttcggatcccaaatatattctgtcctaaggataccgactcattggt 3147

Query: 480 tccctgctcggccacatgcatcattccaggaacactg 516  
|||||  
Sbjct: 3148 tccctgctcggccacatgcatcattccaggaacactg 3184

Score = 95.6 bits (48), Expect = 1e-17  
Identities = 102/120 (85%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcgtcgttaatccctccagatccctggaatgcatgagcatgcatcaaa 419  
|||||  
Sbjct: 1678 aaacgtaaatcgtcgttaatccctccagatccctggaatgcatgagcatgcatcaaa 1737

Query: 420 gacatccagttcggatcccaaatatattctgtcctaaggataccgactcattggt 479  
|||||  
Sbjct: 1738 gacatccagttcggatcccaaatatattctgtcctaaggataccgactcattggt 1797

Score = 61.9 bits (31), Expect = 2e-07  
Identities = 73/87 (83%)  
Strand = Plus / Plus

Query: 208 ttccatttgcaggccctaccacctaactgagtttgaatttcccatgaggacatc 267  
|||||  
Sbjct: 4235 ttccatttgcaggccctaccacctaactgagtttgaatttcccatgaggacatc 4294

Query: 268 tgaactatgaaatgacgcgcctggttatt 294  
|||||  
Sbjct: 4295 tgaactatgaaatgacgcgcctggttatt 4321

>GSEBQ.ABA91636 Human C3B/CAB receptor CRL (complement receptor type  
1) cDNA.  
Length = 6951

Score = 599 bits (302), Expect = e-169

Identities = 350/366 (95%)  
Strand = Plus / Plus

Query: 185 tcaatgcatgctccggaatgcttccatcttgcaggcctcaacaactaatgactt 244  
|||||  
Sbjct: 150 tcaatgcaatgcccagaatgcttccatcttgcaggcctcaacaactaatgactt 209

Query: 245 tgaattcccatggagacatacttgaactaagaatgcgcctctgttatcccggaagcc 304  
|||||  
Sbjct: 210 tgaattcccatggagacatacttgaactaagaatgcgcctctgttatcccggaagcc 269

Query: 305 gtttctatcatctgcccataaaactcagcttggacaagtgtctaagagacaagtccaagc 364  
|||||  
Sbjct: 270 gtttctatcatctgcccataaaactcagcttggactgtgtctaagagaggttcagagc 329

Query: 365 taatcatgctcgttaattcctccagatcctgtgtaatgcatgacacatgtatccaagaacat 424  
|||||  
Sbjct: 330 taatcatgctcgttaattcctccagatcctgtgtaatgcatgacacatgtatccaagaacat 389

Query: 425 ccagttcggatcccaatttaaatatctctgtcctaagaagataccagcatctgttccctc 484  
|||||  
Sbjct: 390 ccagttcggatcccaatttaaatatctctgtcctaagaagataccagcatctgttccctc 449

Query: 485 gtctgccatgcatcatcctccaggaacacacgtcattgttgataataaacctctgttg 544  
|||||  
Sbjct: 450 gtctgccatgcatcatcctccaggaacacacgtcattgttgataataaacctctcttg 509

Query: 545 tgacag 550  
|||||  
Sbjct: 510 tgacag 515

Score = 97.6 bits (49), Expect = 3e-18  
Identities = 130/157 (82%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgtcgttaactctccagatccctgtgaatggcatggcacatgfatcaaa 419  
|||||  
Sbjct: 3025 aaacgtaaatcatgttaaaactctccagatccctgtgaatggcatggcacatgfatcaaa 3084

Query: 420 gacatccagttcggatcccaatttaaatatcttgccttaagaagatacgaacatcttgt 479  
|||||  
Sbjct: 3085 gacatccagttcggatcccaatttaaatatcttgccttaagaagatacgaacatcttgt 3144

Query: 480 tctctgctggcacatgcatcatctcaggaacactg 516  
|||||  
Sbjct: 3145 cactcatcgtcgaatgtatcctctcaggaacactg 3181

Score = 95.6 bits (48), Expect = 1e-17  
Identities = 102/120 (85%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgtcgttaactctccagatccctgtgaatggcatggcacatgfatcaaa 419

|||||  
Sbjct: 1675 aaacgtaaatcatgttaaaactctccagatccctgtgaatggcatggtcgtatcaca 1734

Query: 420 gacatccagttcggatcccaatttaaatatcttgccttaagaagatacgaactatctgt 479  
|||||  
Sbjct: 1735 gacatccagttcggatcccaatttaaatatcttgccttaagaagatacgaactatctgt 1794

Score = 61.9 bits (31), Expect = 2e-07  
Identities = 73/87 (83%)  
Strand = Plus / Plus

Query: 208 ttccatttgcaggcctcaacaacttaactgatatgttgaatttcccatgtgacatacc 267  
|||||  
Sbjct: 4232 ttccatttgcaggcctcaagaatcccaatttaactgatatgttgaatttcccatgtgacatacc 4291

Query: 268 tgaactaagaatgcgcctctgttact 294  
|||||  
Sbjct: 4292 tgaactaagaatgcgcctctgttact 4318

>GSE01ABX84738 Human cDNA differentially expressed in granulocytic  
cells #1309.  
Length = 6951

Score = 599 bits (302), Expect = e-169  
Identities = 350/366 (95%)  
Strand = Plus / Plus

Query: 185 tcaatgcaatgctccggaatgcttccatcttgcaggcctcaacaactaatgactt 244  
|||||  
Sbjct: 150 tcaatgcaatgctccggaatgcttccatcttgcaggcctcaacaactaatgactt 209

Query: 245 tgaattcccatggagacatacttgaactaagaatgcgcctctgttatcccggaagacc 304  
|||||  
Sbjct: 210 tgaattcccatggagacatacttgaactaagaatgcgcctctgttatcccggaagacc 269

Query: 305 gtttctatcatctgcccataaaactcagcttggacaagtgtctaagagacaagtgcacaagc 364  
|||||  
Sbjct: 270 gtttctatcatctgcccataaaactcagcttggactgtgtctaagagacaagtgcagagc 329

Query: 365 taatcatgctcgttaattcctccagatcctgtgtaatgcatggcacatgfatccaagaacat 424  
|||||  
Sbjct: 330 taatcatgctcgttaattcctccagatcctgtgtaatgcatggcacatgfatccaagaacat 389

Query: 425 ccagttcggatcccaatttaaatatcttgccttaagaagatacgaactatctgttcctc 484  
|||||  
Sbjct: 390 ccagttcggatcccaatttaaatatcttgccttaagaagatacgaactatctgttcctc 449

Query: 485 gtctgccatgcatcatcctccaggaacacacgtcattgttgataataaacacactcttg 544  
|||||  
Sbjct: 450 gtctgccatgcatcatcctccaggaacacacgtcattgttgataataaacacactcttg 509

Query: 545 tgacag 550  
|||||

Sbjct: 510 tgacag 515

Score = 97.6 bits (49), Expect = 3e-18  
Identities = 130/157 (82%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgctgtaaatccctccagatccctgtaattggatggcatggcacatgtaacaa 419

Sbjct: 3025 aaacgtaaatcatgtaaaactccctccagatccagtgaaatggcatgggtgcatgtaacacaa 3084

Query: 420 gacatccagttcgatgcccaatlaattatcttgcctaaaggataccgacatcattggt 479

Sbjct: 3085 gacatccagttcgatgcccaatlaattatcttgcctaaaggataccgacatcattggt 3144

Query: 480 tccctgctgcacatgcatcatcctcaggaacacatg 516

Sbjct: 3145 cactcatctgctgaaatgtaatccctccaggaacacatg 3181

Score = 95.6 bits (48), Expect = 1e-17  
Identities = 102/120 (85%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgctgtaaatccctccagatccctgtaattggatggcatggcacatgtaacaa 419

Sbjct: 1675 aaacgtaaatcatgtaaaactccctccagatccagtgaaatggcatgggtgcatgtaacaa 1734

Query: 420 gacatccagttcgatgcccaatlaattatcttgcctaaaggataccgacatcattggt 479

Sbjct: 1735 gacatccagttcgatgcccaatlaattatcttgcctaaaggataccgacatcattggt 1794

Score = 61.9 bits (31), Expect = 2e-07  
Identities = 73/87 (83%)  
Strand = Plus / Plus

Query: 208 ttccatttgcagagccctacacaaatlaattatcttgcctaaaggataccgacatcattggt 267

Sbjct: 4232 ttccatttgcagagccctacacaaatlaattatcttgcctaaaggataccgacatcattggt 4291

Query: 268 tgaactatgaatgcgcctctggttaatt 294

Sbjct: 4292 tgaactatgaatgcgcctctggttaatt 4318

>GSEQ:AI58380 Human polynucleotide SEQ ID NO 583.  
Length = 7313

Score = 599 bits (302), Expect = e-169  
Identities = 350/366 (95%)  
Strand = Plus / Plus

Query: 185 tcaatgcatgtcccggaatggcttccatttgcagggcctaccacaaactaactgatact 244

Sbjct: 150 tcaatgcatgtcccggaatggcttccatttgcagggcctaccacaaactaactgatact 209

Query: 245 tgaatttccattggagacatactgaaactgaatgcgcctctgtaattccggaaagacc 304  
Sbjct: 210 tgaatttccattggagacatactgaaactgaatgcgcctctgtaattccggaaagacc 269

Query: 305 gtttctatcatctgctcctaaaaactcagcttgagacagtgctaaaggatacggacagc 364  
Sbjct: 270 gtttctatcatctgctcctaaaaactcagcttgagacagtgctaaaggatacggacagc 329

Query: 365 taatcatgctgtaactcctccagatccctgtaattggcatggcatgtaataaagacat 424  
Sbjct: 330 taatcatgctgtaactcctccagatccctgtaattggcatggcatgtaataaagacat 389

Query: 425 ccagttcgatcccaatlaattatcttgcctaaaggataccgacatcattggttccct 484  
Sbjct: 390 ccagttcgatcccaatlaattatcttgcctaaaggataccgacatcattggttccct 449

Query: 485 gtctgcaacatgatactcctcaggaacacatgctatttggataataaacacctggttg 544  
Sbjct: 450 gtctgcaacatgatactcctcaggaacacatgctatttggataataaacacacattcgg 509

Query: 545 tgacag 550  
Sbjct: 510 tgacag 515

Score = 97.6 bits (49), Expect = 3e-18  
Identities = 130/157 (82%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgctgtaaatccctccagatccctgtaattggatggcatggcacatgtaacaa 419

Sbjct: 3025 aaacgtaaatcatgtaaaactccctccagatccagtgaaatggcatgggtgcatgtaacaa 3084

Query: 420 gacatccagttcgatgcccaatlaattatcttgcctaaaggataccgacatcattggt 479

Sbjct: 3085 gacatccagttcgatgcccaatlaattatcttgcctaaaggataccgacatcattggt 3144

Query: 480 tccctgctgcacatgcatcatcctcaggaacacatg 516

Sbjct: 3145 cactcatctgctgaaatgtaatccctccaggaacacatg 3181

Score = 95.6 bits (48), Expect = 1e-17  
Identities = 102/120 (85%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgctgtaaatccctccagatccctgtaattggatggcatggcacatgtaacaa 419

Sbjct: 1675 aaacgtaaatcatgtaaaactccctccagatccagtgaaatggcatgggtgcatgtaacaa 1734

Query: 420 gacatccagttcgatgcccaatlaattatcttgcctaaaggataccgacatcattggt 479  
Sbjct: 1735 gacatccagttcgatgcccaatlaattatcttgcctaaaggataccgacatcattggt 1794

Score = 61.9 bits (31), Expect = 2e-07  
Identities = 73/87 (83%)  
Strand = Plus / Plus

Query: 208 ttccatttcgagcgcctaccacctaactgaactgaacttgaatttccattggagacatc 267  
Sbjct: 4232 ttccatttcgagcgcctaccacctaactgaactgaacttgaatttccattggagacatc 267

Query: 268 tgaactatgaatgccgcctctgtatc 294  
Sbjct: 4292 tgaactatgaatgccgcctctgtatc 4318

>GSEQ:AA238150 Human C3b/C4b receptor (CR1) protein encoding DNA.  
Length = 6951

Score = 599 bits (302), Expect = e-169  
Identities = 350/366 (95%)  
Strand = Plus / Plus

Query: 185 tcaatgaatgtcccggaatggcttccatttgcagggcctaccacctaactgaatgactc 244  
Sbjct: 150 tcaatgaatgtcccggaatggcttccatttgcagggcctaccacctaactgaatgactc 209

Query: 245 tgaatttccattggagacatactgaactatgaatgcgcgcctgtatctccggaagacc 304  
Sbjct: 210 tgaatttccattggagacatactgaactatgaatgcgcgcctgtatctccggaagacc 269

Query: 305 gtcttcattcatctgcctaaataaactcagctcgtgacaagtcgaagaagtcgaagc 364  
Sbjct: 270 gtcttcattcatctgcctaaataaactcagctcgtgacaagtcgaagaagtcgaagc 329

Query: 365 taatcatgtcgttaatcctcccaagatcctggaatggcatggacatggatccaagacat 424  
Sbjct: 330 taatcatgtcgttaatcctcccaagatcctggaatggcatggatccaagacat 389

Query: 425 ccagttcggatcccaataataatcttgcctaaaggataccggaatcattgttccctc 484  
Sbjct: 390 ccagttcggatcccaataataatcttgcctaaaggataccggaatcattgttccctc 449

Query: 485 gtctgcacatgcatactcccaagcaaacactgtcatttgggataataaacactgtttg 544  
Sbjct: 450 gtctgcacatgcatactcccaagcaaacactgtcatttgggataataaacactgtttg 509

Query: 545 tgacag 550  
Sbjct: 510 tgacag 515

Score = 97.6 bits (49), Expect = 3e-18  
Identities = 130/157 (82%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgtcgttaatcctccagatcctgtgaatggatggacatgtgatacaa 419

Sbjct: 3025 aaacgtaaatcatgttaaacctccctccagatccagtggaatggatggatgtgatacaa 3084

Query: 420 gacatccagttcggatcccaataataatcttgcctaaaggataccggaatcattggt 479  
Sbjct: 3085 gacatccagttcggatcccaataataatcttgcctaaaggataccggaatcattggt 3144

Query: 480 tccctgcctccacatgcatcatcctcaggcaacagc 516  
Sbjct: 3145 cactcatcctgcatgcatcctcctccaggcaatctagc 3181

Score = 95.6 bits (48), Expect = 1e-17  
Identities = 102/120 (85%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgtcgttaatcctccagatccttgaatggcatggacatgtgatacaa 419  
Sbjct: 1675 aaacgtaaatcatgttaaacctccctccagatccagtggaatggatgtgatacaa 1734

Query: 420 gacatccagttcggatcccaataataatcttgcctaaaggataccggaatcattggt 479  
Sbjct: 1735 gacatccagttcggatcccaataataatcttgcctaaaggataccggaatcattggt 1794

Score = 61.9 bits (31), Expect = 2e-07  
Identities = 73/87 (83%)  
Strand = Plus / Plus

Query: 208 ttccatttgcagggcctaccacctaactgaatgacttgaatttccattggagacatc 267  
Sbjct: 4232 ttccatttgcagggcctaccacctaactgaatgacttgaatttccattggagacatc 4291

Query: 268 tgaactatgaatgcgcctctgtatc 294  
Sbjct: 4292 tgaactatgaatgcgcctctgtatc 4318

>GSEQ:AAQ11642 Entire human complement type 1 receptor coding region.  
Length = 6951

Score = 599 bits (302), Expect = e-169  
Identities = 350/366 (95%)  
Strand = Plus / Plus

Query: 185 tcaatgaatgtcccggaatggcttccatttgcagggcctaccacctaactgaatgactc 244  
Sbjct: 150 tcaatgaatgtcccggaatggcttccatttgcagggcctaccacctaactgaatgactc 209

Query: 245 tgaatttccattggagacatactgaactatgaatgcgcgcctgtatctccggaagacc 304  
Sbjct: 210 tgaatttccattggagacatactgaactatgaatgcgcgcctgtatctccggaagacc 269

Query: 305 gtcttcattcatctgcctaaataaactcagctcgtgacaagtcgaagaagtcgaagc 364  
Sbjct: 270 gtcttcattcatctgcctaaataaactcagctcgtgacaagtcgaagaagtcgaagc 329

Sbjct: 270 gttttctatcatctgtcctaaataaacctcagctcgtgacgtgctgaagagacaggtgcagacg 329

Query: 365 taatcatctgttaatccctccagatcccttgtaatgagatgcacatgtgatcaagaagacat 424  
|||||

Sbjct: 330 taatcatctgttaatccctccagatcccttgtaatgagatgcacatgtgatcaagaagacat 389

Query: 425 ccagctcggatccccaattaaataatctctgtccctaaagataccgactcatctgttctctc 484  
|||||

Sbjct: 390 ccagctcggatccccaattaaataatctctgtctaaagataccgactcatctgttctctc 449

Query: 485 gtctgcacatgcatcatcttcacaggaacactgtcatcttggaataaaccactgtttcg 544  
|||||

Sbjct: 450 gtctgcacatgcatcatcttcacaggtgatcatcttggaataaaccactatttg 509

Query: 545 tgacag 550  
|||||

Sbjct: 510 tgacag 515

Score = 97.6 bits (49), Expect = 3e-18  
Identities = 130/157 (82%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgtcgttaatccctccagatcccttgtaatgagatgcacatgtgatcaaa 419  
|||||

Sbjct: 3025 aaacgtaaatcatgttaaatccctccagatcccttgtaatgagatgcacatgtgatcaaa 3084

Query: 420 gacatccagctcggatccccaattaaataatctctgtccctaaagataccgactcatctgt 479  
|||||

Sbjct: 3085 gacatccagctcggatccccaattaaataatctctgtcactaaagataccgactcatctgt 3144

Query: 480 tccctcgtctgcacatgcatcatcttcacaggaacactg 516  
|||||

Sbjct: 3145 cactcatctgtcgaatgcatctctccaggaacactg 3181

Score = 95.6 bits (48), Expect = 1e-17  
Identities = 102/120 (85%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgtcgttaatccctccagatcccttgtaatgagatgcacatgtgatcaaa 419  
|||||

Sbjct: 1675 aaacgtaaatcatgttaaatccctccagatcccttgtaatgagatgcacatgtgatcaaa 1734

Query: 420 gacatccagctcggatccccaattaaataatctctgtccctaaagataccgactcatctgt 479  
|||||

Sbjct: 1735 gacatccagctcggatccccaattaaataatctctgtcactaaagataccgactcatctgt 1794

Score = 61.9 bits (31), Expect = 2e-07  
Identities = 73/87 (83%)  
Strand = Plus / Plus

Query: 208 ttccatttgcagagccttaaccaactcatgtacttggaatttccattggagacatc 267  
|||||

Sbjct: 4232 ttccatttgcagagccttaaccaactcatgtacttggaatttccattggagacatc 4291

Query: 268 tgaactatgaatgcgcgccttggttact 294  
|||||

Sbjct: 4292 tgaactatgaatgcgcgccttggttact 4318

>GSEQ:AM91477 CRI protein DNA.  
Length = 6951

Score = 599 bits (302), Expect = e-169  
Identities = 350/366 (95%)  
Strand = Plus / Plus

Query: 185 tcaatgcaatgtcccggaatgtctccatttgcagagccttaaccaactcatgtgagtc 244  
|||||

Sbjct: 150 tcaatgcaatgtcccggaatgtctccatttgcagagccttaaccaactcatgtgagtc 209

Query: 245 tgaatttcccatctggagacatctgaactatgaatgcgcgccttggttattcccgagacc 304  
|||||

Sbjct: 210 tgaatttcccatctggagacatctgaactatgaatgcgcgccttggttattcccgagacc 269

Query: 305 gttttctatcatctgtccctaaataaacctcagctcgtgacaggtgtctaaggaacaggtgcagc 364  
|||||

Sbjct: 270 gttttctatcatctgtccctaaataaacctcagctcgtgacaggtgtctaaggaacaggtgcagc 329

Query: 365 taatcatctgttaatccctccagatcccttgtaatgagatgcacatgtgatcaagaacat 424  
|||||

Sbjct: 330 taatcatctgttaatccctccagatcccttgtaatgagatgcacatgtgatcaagaacat 389

Query: 425 ccagctcggatccccaattaaataatctctgtccctaaagataccgactcatctgttctctc 484  
|||||

Sbjct: 390 ccagctcggatccccaattaaataatctctgtcactaaagataccgactcatctgttctctc 449

Query: 485 gtctgcacatgcatcatcttcacaggaacactgtcatcttggaataaaccactgtttcg 544  
|||||

Sbjct: 450 gtctgcacatgcatcatcttcacaggtgatcatcttggaataaaccactatttg 509

Query: 545 tgacag 550  
|||||

Sbjct: 510 tgacag 515

Score = 97.6 bits (49), Expect = 3e-18  
Identities = 130/157 (82%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcatgtcgttaatccctccagatcccttgtaatgagatgcacatgtgatcaaa 419  
|||||

Sbjct: 3025 aaacgtaaatcatgttaaatccctccagatcccttgtaatgagatgcacatgtgatcaaa 3084

Query: 420 gacatccagctcggatccccaattaaataatctctgtccctaaagataccgactcatctgt 479  
|||||

Sbjct: 3085 gacatccagctcggatccccaattaaataatctctgtcactaaagataccgactcatctgt 3144

Query: 480 tcctcgtctgcacatgcacatcatctcagcgaactg 516  
|||||  
Sbjct: 3145 cactcatcgtctgaatgcacatccctcagcgaactg 3181

Score = 95.6 bits (48), Expect = 1e-17  
Identities = 102/120 (85%)  
Strand = Plus / Plus

Query: 360 aaacgtaaatcatcgtctgtaatccctcagatccctggaatgagcatgacatgtgataaa 419  
|||||  
Sbjct: 1675 aaacgtaaatcatcgttaaaactccctcagatccagtgatgagcatgtgtgtacaca 1734

Query: 420 gacatccagtcgagtcgacccaataatattcttgcctaaagataccgactcattggt 479  
|||||  
Sbjct: 1735 gacatccagtcgagtcgacccaataatattcttgcctaaagatccgactcattggt 1794

Score = 61.9 bits (31), Expect = 2e-07  
Identities = 73/87 (83%)  
Strand = Plus / Plus

Query: 208 ttccattggcagagcctaccacctaactgactgatttgattcccatggacataac 267  
|||||  
Sbjct: 4232 ttccattggcagtcctaccacctaactgactgatttgattcccatggacataac 4291

Query: 268 tgaactatgaatgcgcgccttgattt 294  
|||||  
Sbjct: 4292 tgaactatgaatgcgcgccttgattt 4318

Database: Current: Geneseq\_NA.fasta  
Posted date: Apr 14, 2003 11:38 AM  
Number of letters in database: 1,289,285,926  
Number of sequences in database: 2,461,325

Lambda K H  
1.37 0.711 1.31

Gapped  
Lambda K H  
1.37 0.711 1.31

Matrix: blastn matrix:1 -3  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 466016  
Number of Sequences: 2461325  
Number of Extensions: 466016  
Number of successful extensions: 32593  
Number of sequences better than 10.0: 91  
length of query: 627  
length of database: 1,289,285,926  
effective HSP length: 20  
effective length of query: 607  
effective length of database: 1,240,059,426  
effective search space: 752716071582  
effective search space used: 752716071582  
T: 0  
A: 0

X1: 6 (11.9 bits)  
X2: 10 (19.8 bits)  
S1: 12 (24.3 bits)

Graphical View...

Submit sequences to: BLAST2

